

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 20, 2005, 12:35:04 ; Search time 165 Seconds  
(without alignments)

**Title:** US-10-692-299-2

Perfect score: 589  
Sequence: 1 MFGATRVSIMLLLVTVSDCA.....CSRPDGRYRCNDLKNINF 105

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : A_Geneseq_16Dec04.*
1: Genesexp1980s.*
2: Genesexp1990s.*
3: Genesexp2000s.*
4: Genesexp2001s.*
5: Genesexp2002s.*
6: Genesexp2003as.*
7: Genesexp2003bs.*
8: Genesexp2004s.*
```

## SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length	†			
1	589	100.0	105	3	AAV66745	AAV66745 Membrane-	
2	589	100.0	105	3	AAEL18453	AAEL18453 A Human T	
3	589	100.0	105	4	AAAB70148	AAAB70148 Human G p	
4	589	100.0	105	4	AAAB68427	AAAB68427 Amino aci	
5	589	100.0	105	4	AAU12406	AAU12406 Human PRO	
6	589	100.0	105	4	AAAB53096	AAAB53096 Human ang	
7	589	100.0	105	4	AAAB65268	AAAB65268 Human PRO	
8	589	100.0	105	4	AAAB48175	AAAB48175 Human PRO	
9	589	100.0	105	4	AAAB48067	AAAB48067 Human ext	
10	589	100.0	105	5	AAAM50773	AAAM50773 Endocrine	
11	589	100.0	105	5	AAUB3674	AAUB3674 Human PRO	
12	589	100.0	105	5	AAAB84902	AAAB84902 Human PRO	
13	589	100.0	105	5	AAOL15527	AAOL15527 Human phy	
14	589	100.0	105	5	ABBO6308	ABBO6308 Human G p	
15	589	100.0	105	5	AAE24382	AAE24382 Human pro	
16	589	100.0	105	5	ABBY95508	ABBY95508 Human ang	
17	589	100.0	105	6	ABU58083	ABU58083 Human PRO	
18	589	100.0	105	6	ABU59161	ABU59161 Novel hum	
19	589	100.0	105	6	ABU82673	ABU82673 Human sec	
20	589	100.0	105	6	ABOI17850	ABOI17850 Novel hum	
21	589	100.0	105	6	ABU60592	ABU60592 Human sec	
22	589	100.0	105	6	ABU080821	ABU080821 Human PRO	
23	589	100.0	105	6	ABO33787	ABO33787 Novel hum	
24	589	100.0	105	6	ABU13974	ABU13974 Human PRO	
25	589	100.0	105	6	ABU08800	ABU08800 Human end	

## ALIGNMENTS

RESULT 1	
AAAY66745	
ID	AAAY66745 standard; protein; 105 AA.
XX	
AC	AAAY66745;
XX	
DT	05-APR-2000 (first entry)
XX	
DE	Membrane-bound protein PRO1186.
XX	
KW	Membrane-bound polypeptide; PRO pol
KW	pharmaceutical; receptor immunoadhe
XX	
OS	Homo sapiens.
XX	
FN	WO9963088-A2.
XX	
PD	09-DEC-1999.
XX	
PF	02-JUN-1999; 99NO-US012252.
XX	
PR	02-JUN-1998; 98US-0087607P.
PR	02-JUN-1998; 98US-0087609P.
PR	02-JUN-1998; 98US-0087759P.
PR	03-JUN-1998; 98US-0087827P.
PR	04-JUN-1998; 98US-0088021P.
PR	04-JUN-1998; 98US-0088025P.
PR	04-JUN-1998; 98US-0088028P.
PR	04-JUN-1998; 98US-0088029P.
PR	04-JUN-1998; 98US-0088030P.
PR	04-JUN-1998; 98US-0088033P.
PR	04-JUN-1998; 98US-0088325P.
PR	05-JUN-1998; 98US-0088167P.
PR	05-JUN-1998; 98US-0088202P.
PR	05-JUN-1998; 98US-0088212P.
PR	05-JUN-1998; 98US-0088217P.
PR	09-JUN-1998; 98US-0088555P.
PR	10-JUN-1998; 98US-0088722P.
PR	10-JUN-1998; 98US-0088734P.
PR	10-JUN-1998; 98US-0088738P.
PR	10-JUN-1998; 98US-0088740P.
PR	10-JUN-1998; 98US-0088741P.
PR	10-JUN-1998; 98US-0088742P.
PR	10-JUN-1998; 98US-0088810P.
PR	10-JUN-1998; 98US-0088811P.
PR	10-JUN-1998; 98US-0088824P.
PR	10-JUN-1998; 98US-0088825P.



QY 61 HPGSHKVPFFPRKRKHHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105  
 |||||  
 Db 61 HPGSHKVPFFPRKRKHHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105  
 |||||

RESULT 2  
 AAB18453  
 ID AAB18453 standard; protein; 105 AA.  
 AC AAB18453;  
 XX  
 DT 15-JAN-2001 (first entry)  
 XX  
 DE A human TANGO 266 polypeptide.  
 XX  
 KW TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;  
 KW cellular proliferation; cellular differentiation; cellular adhesion;  
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;  
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;  
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;  
 KW intestinal disorder; spleen associated disease; renal disorder;  
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;  
 KW brain herniation; iatrogenic disease; inflammation; meningitis;  
 KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;  
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.  
 XX  
 OS Homo sapiens.  
 XX

Key Location/Qualifiers  
 Peptide 1..19  
 FT /note= "signal sequence"  
 FT Protein 20..106  
 FT /note= "mature protein"  
 XX  
 PN WO200052022-A1.  
 XX  
 OS 08-SEP-2000.  
 XX  
 XX 01-MAR-2000; 2000WO-US005226.  
 XX  
 PR 01-MAR-1999; 99US-0122458P.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 XX  
 XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;  
 PI  
 XX WPI; 2000-579269/54.  
 DR N-PSDB; AAA75155.  
 XX  
 XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,  
 PT 266 and 267 useful as modulating agents of cellular processes, e.g. for  
 PT treating cancer.  
 XX

Claim 8; Fig 14; 175pp; English.  
 PS  
 XX The present sequence represents a human TANGO 266 polypeptide. The  
 CC specification also describes TANGO 262, TANGO 216, TANGO 261, and TANGO  
 CC 267. The TANGO polypeptides can be used to modulate cellular  
 CC proliferation, modulate cellular differentiation and/or modulate cellular  
 CC adhesion. The proteins can be used to treat any von Willebrand factor-  
 CC associated disorder, regulate extracellular matrix structuring, cellular  
 CC adhesion, and cell trafficking and/or migration, modulate cellular  
 CC interactions, modulate cell adhesion in proliferative disorders, such as  
 CC cancer, modulate the proliferation, differentiation, and/or function of  
 CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,  
 CC blood and hematopoietic associated diseases and disorders, atelectasis,  
 CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial  
 CC asthma and bronchiectasis, intestinal disorders, spleen associated  
 CC diseases, modulate renal disorders, treat cardiovascular disorders such  
 CC as ischemic heart disease, modulate the proliferation, differentiation,  
 CC and/or function of bone and cartilage cells and to treat bone and/or  
 CC cartilage associated diseases or disorder. They may also be used to treat

CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,  
 CC brain herniations, iatrogenic disease, inflammations, bacterial and viral  
 CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's  
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and  
 CC encephalitis, and treat hepatic disorders  
 XX  
 SQ Sequence 105 AA;  
 Query Match 100.0%; Score 589; DB 3; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-54;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

QY 1 MRGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMTCTPLGREGEC 60  
 |||||  
 Db 1 MRGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMTCTPLGREGEC 60  
 |||||

QY 61 HPGSHKVPFFPRKRKHHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105  
 |||||  
 Db 61 HPGSHKVPFFPRKRKHHTCPCLPNLLCSRPDPGRYRCMDLKNINF 105  
 |||||

RESULT 3  
 AAB70148  
 ID AAB70148 standard; protein; 105 AA.  
 XX  
 AC AAB70148;  
 XX  
 DT 29-MAY-2001 (first entry)  
 XX  
 DE Human G protein-coupled receptor protein-related sequence #4.  
 XX  
 KW Human; G protein-coupled receptor protein; nootropic; neuroprotective;  
 KW hypotensive; orexigenic; anti-allergic; anti-anginal; antimicrobial;  
 KW antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia;  
 KW allergy; angina pectoris; infection; MRSA;  
 KW multiple resistant Staphylococcus aureus.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200116309-A1.  
 XX  
 PD 08-MAR-2001.  
 XX  
 PF 24-AUG-2000; 2000WO-JP005685.  
 XX  
 PR 27-AUG-1999; 99JP-00241531.  
 PR 18-JUL-2000; 2000JP-00217474.  
 XX  
 PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX  
 XX Watanabe T, Terao Y, Shintani Y;  
 PI  
 XX WPI; 2001-226684/23.  
 DR  
 XX

New human brain-originated guanosine triphosphate protein-coupled  
 receptor protein, its salt and encoded gene, useful in (gene) diagnosis  
 and development of preventives and remedies for Alzheimer's disease,  
 hypertension and anorexia.  
 XX  
 Example 4; Page 113; 119pp; Japanese.  
 XX  
 The present sequence is provided in a specification relating to a protein  
 or its salt with an amino acid sequence identical or substantially  
 similar to a fully defined sequence of 393 amino acids as given in the  
 specification. The protein is useful in gene diagnosis and development of  
 preventives and remedies for diseases associated with dysfunction of the  
 protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy,  
 angina pectoris and infections (e.g. multiple resistant Staphylococcus  
 aureus). The proteins and DNA encoding the proteins are also useful for  
 the treatment of these diseases by gene therapy  
 XX  
 SQ Sequence 105 AA;

	Query Match	100.0%;	Score 589;	DB 4;	Length 105;
	Best Local Similarity	100.0%;	Pred. No. 3.3e-54;		
	Matches 105;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MRGATRVSIIMLLLVTVSDCAVITGACERDVQCAGTCCAISLWLRGLRMCTPLGRBGEEC	60		
Db	1	MRGATRVSIIMLLLVTVSDCAVITGACERDVQCAGTCCAISLWLRGLRMCTPLGRBGEEC	60		
Qy	61	HPGSHKVPPFRKRGHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF	105		
Db	61	HPGSHKVPPFRKRGHHTCPCLPNLLCSRFPDGRYRCSDMLKNINF	105		

RESULT 4	
AAB68427	AAB68427 standard; protein; 105 AA.
XX	
XX	
AC	
AC	
XX	
XX	
DT	23-JUL-2001 (first entry)
XX	
XX	
DE	Amino acid sequence of a human Zven2 polypeptide.
XX	
KW	Zven1; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing;
KW	antitumour; antiinflammatory; necrosis; tissue growth; digestive enzyme;
KW	cellular differentiation; gastrointestinal cell contractility;
KW	gastrointestinal motility; inflammation; hypermotility; diarrhoea;
KW	Crohn's disease.

RESULT 5
AAU12406
ID AAU12406 standard; protein; 105 AA.
XX AC AAU12406;
XX DT 24-OCT-2001 (first entry)
XX DE Human PRO1186 polypeptide sequence.
XX KW Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast;
KW prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage;
KW ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte;
XX A-peptide; factor VIIA; gene therapy.
XX OS Homo sapiens.
XX PN WO200140466-A2.
XX PD 07-JUN-2001.
XX PF 01-DEC-2000; 2000WO-US032678.
XX PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 02-DEC-1999; 99WO-US028564.
PR 02-DEC-1999; 99WO-US028565.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 20-DEC-1999; 99WO-US030999.
PR 30-DEC-1999; 99WO-US031243.
PR 30-DEC-1999; 99WO-US031274.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000277.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 01-MAR-2000; 2000WO-US005601.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 21-MAR-2000; 2000WO-US007532.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 05-JUN-2000; 2000US-0209832P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 10-NOV-2000; 2000WO-US030873.  
 PA (GETH ) GENENTECH INC.  
 XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
 PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;  
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
 XX WPI: 2001-408281/43.  
 DR N-PSDB; AAS21478.  
 XX Isolated , secretory and transmembrane PRO polypeptide used to detect  
 PT other PRO polypeptides, link bioactive molecules to cells expressing PRO  
 PT polypeptides, and detect the presence of mammalian tumors e.g. lung,  
 PT breast, prostate, cervical.  
 XX Claim 12; Fig 470; 813pp; English.  
 XX AAU12172-AAU12446 represent novel human secretory and transmembrane PRO  
 CC polypeptides. The PRO polypeptides are useful to detect other PRO  
 CC polypeptides, to link bioactive molecules to cells expressing PRO  
 CC polypeptides, to modulate biological activities of cells expressing PRO  
 CC polypeptides, and to detect the presence of mammalian lung, colon,  
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO  
 CC polypeptide expression in a cell sample to that in a control sample. Some  
 CC of the 275 sequences are also useful to stimulate the release of tumour  
 CC necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or  
 CC differentiation of chondrocytes, the proliferation or gene expression in  
 CC pericyte cells, the release of proteoglycans from cartilage, the  
 CC proliferation of inner ear utricular supporting cells or of T-  
 CC lymphocytes, the release of a cytokine from peripheral blood monocytes  
 CC (PBMCs), or the proliferation of endothelial cells. Some of the PRO  
 CC polypeptides may modulate glucose or free fatty acid uptake by skeletal  
 CC muscle cells or by adipocytes; or inhibit binding of A-peptide to factor  
 CC VIIA. The PRO polypeptides can be used in assays to identify molecules  
 CC involved in binding interactions. The polynucleotides encoding PRO  
 CC polypeptides can be used to generate probes, antisense RNA/DNA,  
 CC transgenic or knock out animals and can be used in gene therapy  
 XX Sequence 105 AA;  
 SQ Query Match 100.0%; Score 589; DB 4; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-54;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MRGATRVSIIMLLVTSDCAVITGACERDVQCGAGTCCALSLMLRGLRMTPLGREGEC 60  
 Db 1 MRGATRVSIIMLLVTSDCAVITGACERDVQCGAGTCCALSLMLRGLRMTPLGREGEC 60  
 Qy 61 HPGSHKVPFRKRKHHTCPCLNLLCSRFDPGRYRCSDMLKNINF 105  
 Db 61 HPGSHKVPFRKRKHHTCPCLNLLCSRFDPGRYRCSDMLKNINF 105  
 RESULT 6  
 AAB53096  
 ID AAB53096 standard; protein; 105 AA.  
 XX AC AAB53096;  
 DT 28-FEB-2001 (first entry)  
 XX Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.  
 XX Human; angiogenesis-associated protein; PRO; endothelial cell growth;  
 KW cardiac hypertrophy; cardiovascular disorder; endothelial disorder;  
 KW angiogenic disorder; atherosclerosis; osteoporosis; hypertension;  
 KW myocardial infarction; diabetic retinopathy; rheumatoid arthritis;  
 KW Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer;  
 KW Alzheimer's disease; Huntington's disease; stroke; drug screening;  
 KW gene therapy; transgenic animal.

XX Homo sapiens.  
 OS WO2000053753-A2.  
 PN 14-SEP-2000.  
 XX 05-JAN-2000; 2000WO-US000219.  
 XX 08-MAR-1999; 99WO-US005028.  
 PR 12-MAR-1999; 99US-0123957P.  
 PR 14-MAY-1999; 99US-0134287P.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.  
 PR 01-SEP-1999; 99WO-US020111.  
 PR 08-SEP-1999; 99WO-US020594.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 05-OCT-1999; 99WO-US023089.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028409.  
 PR 02-DEC-1999; 99WO-US028564.  
 PR 02-DEC-1999; 99WO-US028565.  
 XX (GETH ) GENENTECH INC.  
 XX Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Kuo SS, Mark MR, Marsters SA;  
 PI Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;  
 XX WPI: 2001-090793/10.  
 DR N-PSDB; AAC97496.  
 XX New isolated nucleic acid for producing a PRO polypeptide, analyzing  
 PT genetic disorders and treating cardiovascular, endothelial or angiogenic  
 PT disorders, such as atherosclerosis, wounds or cancer.  
 XX Claim 69; Fig 66; 293pp; English.  
 XX The invention relates to novel human angiogenesis-associated proteins  
 CC designated PRO proteins (AAB53064-B53097), and to nucleic acids encoding  
 CC PRO proteins. The invention also relates to vectors and host cells  
 CC comprising a PRO nucleic acid, the recombinant production of a PRO  
 CC protein, PRO antibodies specific for a PRO protein, fusion proteins  
 CC comprising a PRO protein, agonists or antagonists of a PRO protein, and  
 CC compounds which inhibit the expression of a PRO gene. The invention  
 CC additionally encompasses methods of identifying modulators of PRO  
 CC expression or activity; diagnosing a cardiovascular, endothelial or  
 CC angiogenic disorder, or a susceptibility to such a disorder by detecting  
 CC mutations in a PRO gene, or the expression level of a PRO gene within a  
 CC particular tissue; treating a cardiovascular, endothelial or angiogenic  
 CC disorder via the administration of a PRO protein, PRO nucleic acid, or  
 CC PRO agonist or antagonist; a retroviral gene therapy vector comprising a  
 CC PRO nucleic acid; and methods of inhibiting or stimulating endothelial  
 CC cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the  
 CC administration of a PRO protein, or an agonist or antagonist thereof. PRO  
 CC nucleic acids, PRO proteins, antibodies against PRO proteins, PRO  
 CC agonists and PRO antagonists may be used as therapeutic agents to treat  
 CC cardiovascular, endothelial or angiogenic disorders, such as  
 CC atherosclerosis, osteoporosis, myocardial infarction, hypertension,  
 CC diabetic retinopathy, rheumatoid arthritis, Crohn's disease, psoriasis,  
 CC endometriosis, ulcers, wounds, cancer, Alzheimer's disease, Huntington's  
 CC disease, or stroke. PRO nucleic acids are additionally useful in the  
 CC recombinant production of PRO proteins, as hybridisation probes to screen  
 CC libraries to isolate cDNAs with sequence identity to PRO proteins, to map  
 CC genes encoding PRO proteins, to analyse genetic disorders, and in gene  
 CC therapy. PRO nucleic acids can also be used to produce transgenic animals  
 CC useful for the development and screening of potential therapeutic agents.  
 CC The present sequence represents a PRO protein of the invention  
 XX Sequence 105 AA;

```
Query Match      100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
   |||||
DB 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
   |||||
QY 61 HPGSHKVPFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF 105
   |||||
DB 61 HPGSHKVPFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF 105
   |||||

RESULT 7
AAB65268
ID AAB65268 standard; protein; 105 AA.
XX
AC AAB65268;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.
XX
DE Human; secreted and transmembrane protein; PRO; cytotstatic; cell death;
XX
KW cancer; chromosomal mapping; gene mapping; tissue typing;
XX
KW diagnostic assay.
XX
OS Homo sapiens.
XX
PN W0200073454-A1.
XX
PD 07-DEC-2000.
XX
PF 30-MAR-2000; 2000WO-US008439.
XX
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
PR 07-JUL-1999; 99US-0143048P.
PR 20-JUL-1999; 99US-0144758P.
PR 26-JUL-1999; 99US-0145698P.
PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99US-05021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 03-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
XX
PA (GETH ) GENENTECH INC.
XX
PI Ashkenazi AJ, Baker KP, Botstein D, Deanoyers L, Eaton DL;
PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX
DR WPI; 2001-032160/04.
DR N-PSDB; AAF44237.
XX
XX PRO polynucleotides used to produce polypeptides used to target bioactive
```

```
PT molecules such as toxins, radiolabels or antibodies, to specific cells,
PT to cause targeted cell death.
XX
PS Claim 12; Fig 266; 935pp; English.
XX
CC The present invention describes human secreted and transmembrane PRO
CC proteins. The PRO proteins have cytotstatic activity. The PRO proteins can
CC be used for targeted delivery of bioactive molecules, such as toxins,
CC radiolabels or antibodies, that cause cell death. PRO nucleotide
CC sequences, and their fragments, can be used as hybridisation probes, in
CC chromosomal and gene mapping, and in the generation of anti-sense RNA and
CC DNA. They may also be used to produce transgenic animals which are used
CC to develop and screen therapeutically useful reagents. The PRO nucleotide
CC and protein sequence can be used for tissue typing and in treating
CC cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to
CC AAF44470 represent PCR primers and hybridisation probes used in the
CC isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to
CC AAB65300 represent human PRO polynucleotide and protein sequences given
CC in the exemplification of the present invention
XX
SQ Sequence 105 AA;

Query Match      100.0%; Score 589; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.3e-54;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
   |||||
DB 1 MRGATRVSIMLLLVTSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGEC 60
   |||||
QY 61 HPGSHKVPFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF 105
   |||||
DB 61 HPGSHKVPFRKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF 105
   |||||

RESULT 8
AAB48175
ID AAB48175 standard; protein; 105 AA.
XX
AC AAB48175;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1186 polypeptide.
XX
KW PRO1186; PRO184; neoplastic; cell growth; tumour; cancer; breast;
KW ovarian; renal; colorectal; uterine; prostate; lung; melanoma;
KW central nervous system; leukemia; antitumor; cytostatic.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..19 /note= "signal sequence"
FT Protein 20..105 /note= "mature protein"
FT Modified-site 33..39 /note= "N-myristoylation site"
FT Modified-site 35..41 /note= "N-myristoylation site"
FT Modified-site 46..52 /note= "N-myristoylation site"
FT Modified-site 88..95 /note= "tyrosine kinase phosphorylation site"
XX
XX W0200075327-A1.
XX
PD 14-DEC-2000.
XX
PF 24-FEB-2000; 2000WO-US004914.
XX
XX 02-JUN-1999; 99WO-US012252.
PR 26-JUL-1999; 99US-0145698P.
```









CC The PRO polypeptides are useful for diagnosing tumours, especially lung  
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or  
 CC liver tumour. The PRO polypeptides are useful for stimulating the  
 CC proliferation of, or gene expression, in pericyte cells, for stimulating  
 CC the proliferation or differentiation of chondrocyte cells, for  
 CC stimulating the release of tumour necrosis factor-alpha from human blood,  
 CC for stimulating or inhibiting the proliferation of normal human dermal  
 CC fibroblast cells. The PRO polypeptide may also be used as molecular  
 CC weight markers and for tissue typing. The PRO nucleic acids have  
 CC applications in molecular biology, including use as hybridisation probes,  
 CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO  
 CC protein sequences of the invention

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 5; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-54;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTCTPLRGEGEC 60  
 |||||  
 Db 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTCTPLRGEGEC 60  
 |||||  
 QY 61 HPGSHKVPFRKRKHHTCTCLPMLCSRFPDGRYRCMDLKNINF 105  
 |||||  
 Db 61 HPGSHKVPFRKRKHHTCTCLPMLCSRFPDGRYRCMDLKNINF 105  
 |||||

RESULT 12

ABB84902  
 ID ABB84902 standard; protein; 105 AA.

XX AC ABB84902;

XX DT 16-MAY-2002 (first entry)

XX DE Human PRO1186 protein sequence SEQ ID NO:172.

XX Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;  
 KW vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;  
 KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;  
 KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;  
 KW age-related macular degeneration; arterial restenosis; angina;  
 KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;  
 KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;  
 KW wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX PN WO200200690-A2.

XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US019692.

XX PR 23-JUN-2000; 2000US-0213637P.

XX PR 20-JUL-2000; 2000US-0219556P.

XX PR 25-JUL-2000; 2000US-0220624P.

XX PR 28-JUL-2000; 2000US-0220864P.

XX PR 02-AUG-2000; 2000US-0222695P.

XX PR 17-AUG-2000; 2000US-00643657.

XX PR 23-AUG-2000; 2000WO-US023522.

XX PR 24-AUG-2000; 2000WO-US023328.

XX PR 07-SEP-2000; 2000US-0230378P.

XX PR 18-SEP-2000; 2000US-00664610.

XX PR 19-SEP-2000; 2000US-00665350.

XX PR 24-OCT-2000; 2000US-0242922P.

XX PR 08-NOV-2000; 2000US-00709238.

XX PR 10-NOV-2000; 2000WO-US030952.

XX PR 01-DEC-2000; 2000WO-US030873.

XX PR 20-DEC-2000; 2000US-00747259.

PR 20-DEC-2000; 2000WO-US034956.  
 PR 22-JAN-2001; 2001US-00767609.  
 PR 28-FEB-2001; 2001US-00796498.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-MAR-2001; 2001WO-US008666.  
 PR 09-MAR-2001; 2001US-00802706.  
 PR 14-MAR-2001; 2001US-00808689.  
 PR 22-MAR-2001; 2001US-00816744.  
 PR 05-APR-2001; 2001US-00828366.  
 PR 10-MAY-2001; 2001US-00854208.  
 PR 10-MAY-2001; 2001US-00854280.  
 PR 25-MAY-2001; 2001US-00866028.  
 PR 25-MAY-2001; 2001US-00866034.  
 PR 30-MAY-2001; 2001WO-US017092.  
 PR 30-MAY-2001; 2001US-00870574.  
 PR 01-JUN-2001; 2001WO-US017443.  
 PR 01-JUN-2001; 2001WO-US017800.  
 XX XX

(GETH ) GENENTECH INC.

Baker KP, Ferrara N, Gerber H, Gerttsen ME, Goddard A;  
 Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

WPI; 2002-090516/12.

DR N-PSDB; ABL88157.

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal.

XX Claim 11; Fig 172; 565pp; English.

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to  
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,  
 CC antiangiogenic, hypotensive, vulnerary and antiarteriosclerotic  
 CC activities, and can be used in gene therapy. The PRO polynucleotides,  
 CC proteins, agonists and antagonists are useful for treating or diagnosing  
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.  
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The PRO polynucleotides have applications in molecular biology,  
 CC including use as hybridisation probes, and in chromosome and gene  
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the  
 CC exemplification of the present invention

XX SQ Sequence 105 AA;

Query Match 100.0%; Score 589; DB 5; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-54;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTCTPLRGEGEC 60  
 |||||

Db 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMTCTPLRGEGEC 60  
 |||||

QY 61 HPGSHKVPFRKRKHHTCTCLPMLCSRFPDGRYRCMDLKNINF 105  
 |||||

Db 61 HPGSHKVPFRKRKHHTCTCLPMLCSRFPDGRYRCMDLKNINF 105  
 |||||

RESULT 13

AAO15527

ID AAO15527 standard; protein; 105 AA.

XX AC AAO15527;

XX DT 24-OCT-2002 (first entry)

XX DE Human physiologically-active 2AQ ligand-related protein 3.

XX XX

KW Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;  
 KW colitis; diarrhoea.  
 XX Homo sapiens.  
 XX WO200257443-A1.  
 XX 25-JUL-2002.  
 XX 21-JAN-2002; 2002WO-JP000378.  
 XX 22-JAN-2001; 2001JP-00013027.  
 XX 17-MAY-2001; 2001JP-00147759.  
 XX (TAKE ) TAKEDA CHEM IND LTD.  
 XX Yamada T, Suenaga M, Nishimura O;  
 XX WPI; 2002-566801/60.  
 XX Industrial production of physiologically-active ZAQ ligand by expressing  
 PT in transformant prokaryote and refolding in redox buffer, for use in  
 PT preventing or treating digestive diseases e.g. colitis and diarrhea.  
 XX Example 3; Page 76-77; 93pp; Japanese.  
 XX The invention comprises a method for producing an active peptide that has  
 CC the same activity as a ZAQ ligand isolated from eukaryotic cells. The  
 CC method of the invention is useful for the production of a physiologically  
 CC -active ZAQ ligand for use in preventing or treating digestive diseases  
 CC (e.g. colitis and diarrhea). The present amino acid sequence represents a  
 CC human physiologically active ZAQ ligand-related protein  
 XX Sequence 105 AA;  
 SQ Query Match 100.0%; Score 589; DB 5; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-54;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEC 60  
 DB 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEC 60  
 QY 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPDGRYRCSMDLKNINF 105  
 DB 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPDGRYRCSMDLKNINF 105  
 RESULT 14  
 ABB06308  
 ID ABB06308 standard; protein; 105 AA.  
 XX ABB06308;  
 AC ABB06308;  
 XX 27-MAY-2002 (first entry)  
 DT Human G protein-coupled receptor ZAQ ligand protein SEQ ID NO:23.  
 DE  
 XX G protein-coupled receptor; ZAQ ligand; physiologically active peptide;  
 KW ZAQ; antidiarrheic; laxative; drug development; digestive disease;  
 KW colitis; diarrhoea; constipation; poor-absorption syndrome; gene therapy.  
 XX Homo sapiens.  
 OS WO200206483-A1.  
 XX 24-JAN-2002.  
 XX 17-JUL-2001; 2001WO-JP006162.  
 XX 18-JUL-2000; 2000JP-00217442.  
 XX 02-FEB-2001; 2001JP-00026779.  
 XX

PA (TAKE ) TAKEDA CHEM IND LTD.  
 XX Ohtaki T, Masuda Y, Takatsu Y, Watanabe T, Terao Y, Shintani Y;  
 PI Hinuma S;  
 XX WPI; 2002-188546/24.  
 DR N-PSDB; ABL49637.  
 XX Physiologically-active peptides from cows milk, useful for developing  
 PT drugs to treat ZAQ-mediated diseases, particularly digestive diseases  
 PT like colitis, diarrhoea, constipation and poor-absorption syndrome, by  
 PT gene therapy.  
 XX Claim 5; Page 61; 191pp; Japanese.  
 PS The present invention describes a peptide containing an amino acid  
 CC sequence (I) identical to or substantially similar to that of the  
 CC sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic and  
 CC laxative activities. The peptides and encoding DNAs from the present  
 CC invention are useful for developing drugs to treat digestive diseases  
 CC like colitis, diarrhoea, constipation and poor-absorption syndrome,  
 CC including gene therapy. The physiologically-active cows milk-originated  
 CC peptides are applicable as a specific ligand of brain-originated orphan G  
 CC protein-coupled receptor protein ZAQ. ABL49615 to ABB40659 and ABB06303  
 CC to ABB06315 represent sequences used in the exemplification of the  
 CC present invention  
 XX Sequence 105 AA;  
 SQ Query Match 100.0%; Score 589; DB 5; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 3.3e-54;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEC 60  
 DB 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGLRMCTPLGREGEC 60  
 QY 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPDGRYRCSMDLKNINF 105  
 DB 61 HPGSHKVPFFRKRKHHTCPLNLLCSRFPDGRYRCSMDLKNINF 105  
 RESULT 15  
 AAE24382  
 ID AAE24382 standard; protein; 105 AA.  
 XX AAE24382;  
 AC AAE24382;  
 XX 04-OCT-2002 (first entry)  
 DT Human prokineticin 1 precursor protein.  
 DE  
 XX Human; prokineticin 1; gastrointestinal motility; intestinal cancer;  
 KW irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea;  
 KW diabetic gastroparesis; chronic constipation; malabsorptive disorder;  
 KW inflammatory bowel disorder; analgesic; infectious disease.  
 XX Homo sapiens.  
 OS Key Location/Qualifiers  
 FH Key 1..19  
 FT Peptide /label= Signal\_peptide  
 FT Protein 20..105  
 FT /note= "Mature human prokineticin 1"  
 XX WO200236625-A2.  
 XX 10-MAY-2002.  
 XX 01-NOV-2001; 2001WO-US047969.  
 XX 03-NOV-2000; 2000US-0245882P.  
 XX

PA (REGC ) UNIV CALIFORNIA.  
XX  
PI Zhou Q, Ehler FJ;  
XX  
DR WPI; 2002-479752/51.  
DR N-PSDB; AAD9321.  
XX  
PT New isolated human prokineticin 1 and 2 polypeptides that stimulate  
PT gastrointestinal smooth muscle contraction, useful for improving impaired  
PT gastrointestinal motility in irritable bowel syndrome, chronic  
PT constipation.  
XX  
PS Example 1; Fig 1; 86pp; English.  
XX  
CC The invention relates to human prokineticin 1 and 2 polypeptides that  
CC stimulate gastrointestinal smooth muscle contraction and nucleic acid  
CC molecules encoding such polypeptides. Polypeptides of the invention are  
CC useful for treating disorders involving impaired gastrointestinal  
CC motility. They are useful for stimulating gastrointestinal motility in  
CC disorders such as irritable bowel syndrome, diabetic gastroparesis, post-  
CC operational ileus, chronic constipation and gastrointestinal reflux  
CC disease. The prokineticin antagonists are useful for inhibiting  
CC gastrointestinal motility in conditions of diarrhoea, malabsorptive  
CC disorders, inflammatory bowel disorders, infectious diseases and  
CC intestinal cancers. The antagonists also act as analgesics. The present  
CC sequence is human prokineticin 1 precursor protein  
XX  
SQ Sequence 105 AA;  
  
Query Match 100.0%; Score 589; DB 5; Length 105;  
Best Local Similarity 100.0%; Pred. NO. 3.3e-54;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db |||||  
1 MRGATRVSNMLLVTVSDCAVITGACERDVQCGAGTCCALSLWRLGLRMCTPLGRGEEC 60  
  
QY 61 HPGSHKVPFFPKRKHHTCPCLPNLLCSRFPDGRYRCMDLKNINF 105  
Db |||||  
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Job time : 167 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

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(without alignments)  
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Title: US-10-692-299-2  
Perfect score: 589  
Sequence: 1 MRGATRVSIMLLLVTSVDC

Scoring table: BLOSUM62  
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
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Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/1/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	589	100.0	105	4	US-09-712-529-5
2	589	100.0	105	4	US-10-212-201A-5
3	589	100.0	105	4	US-10-212-355-5
4	577	98.0	105	4	US-09-621-976-5350
5	448	76.1	80	4	US-09-513-999C-4698
6	303	51.4	108	4	US-09-712-529-2
7	303	51.4	108	4	US-10-212-201A-2
8	303	51.4	108	4	US-10-212-355-2
9	107.5	18.3	224	3	US-09-161-241-14
10	102	17.3	186	4	US-09-949-016-7146
11	102	17.3	207	3	US-09-161-241-13
12	102	17.3	259	3	US-09-161-241-12
13	102	17.3	259	4	US-09-949-016-6872
14	101	17.1	259	3	US-09-161-241-11
15	100.5	17.1	350	3	US-09-161-241-9
16	100.5	17.1	350	4	US-09-907-794A-236
17	100.5	17.1	350	4	US-09-905-125A-236
18	100.5	17.1	350	4	US-09-902-775A-236
19	100.5	17.1	350	4	US-09-906-700-236
20	100.5	17.1	350	4	US-09-903-603A-236
21	100.5	17.1	350	4	US-09-904-920A-236
22	100.5	17.1	350	4	US-09-909-064-236
23	100.5	17.1	350	4	US-09-905-381A-236
24	100.5	17.1	350	4	US-09-906-618-236
25	100.5	17.1	375	4	US-09-949-016-7856
26	100.5	17.1	375	4	US-09-949-016-7857
27	100.5	17.1	375	4	US-09-949-016-7858

28	98.5	16.7	349	3	US-09-161-241-8	Sequence 8, Appli
29	97	16.5	266	3	US-09-161-241-10	Sequence 10, Appli
30	97	16.5	266	4	US-09-976-594-1086	Sequence 1086, Ap
31	82	13.9	1342	4	US-09-561-709B-13	Sequence 13, Appli
32	81	13.8	1964	3	US-09-467-997-1	Sequence 1, Appli
33	79	13.4	124	4	US-09-949-016-11293	Sequence 11293, A
34	78.5	13.3	163	2	US-08-219-237B-5	Sequence 5, Appli
35	78.5	13.3	163	3	US-08-477-347-13	Sequence 13, Appli
36	78.5	13.3	163	3	US-08-476-862-4	Sequence 4, Appli
37	78.5	13.3	163	3	US-08-468-560C-5	Sequence 5, Appli
38	78.5	13.3	163	4	US-09-800-909-4	Sequence 4, Appli
39	78.5	13.3	163	4	US-09-800-908-13	Sequence 13, Appli
40	75.5	12.8	1101	4	US-09-561-709B-5	Sequence 5, Appli
41	75.5	12.8	1761	4	US-09-561-709B-1	Sequence 1, Appli
42	75	12.7	546	4	US-09-949-016-10394	Sequence 10394, A
43	75	12.7	651	1	US-08-264-101-2	Sequence 2, Appli
44	75	12.7	651	2	US-08-765-243-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1  
US-09-712-529-5  
; Sequence 5, Application US/09712529  
; Patent No. 6485938  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Bishop, Paul D.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Thompson, Penny P.  
; TITLE OF INVENTION: Human Zven Proteins  
; FILE REFERENCE: 99-81  
; CURRENT APPLICATION NUMBER: US/09/712,529  
; CURRENT FILING DATE: 2000-11-14  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-712-529-5

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Db	1	MRGATRVSIMLLLVTSVDCAVITGACERDVQCGAGTCCCAISLWLRGRLMCTPLGREGEC	60	
QY	61	HFGSHKVPFRFRKHHKTCCLNLCSPRFDGRCYRCSMDLKNINF	105	
Db	61	HFGSHKVPFRFRKHHKTCCLNLCSPRFDGRCYRCSMDLKNINF	105	

RESULT 2  
US-10-212-201A-5  
; Sequence 5, Application US/10212201A  
; Patent No. 6756479  
; GENERAL INFORMATION:  
; APPLICANT: Sheppard, Paul O.  
; APPLICANT: Bishop, Paul D.  
; APPLICANT: Whitmore, Theodore E.  
; APPLICANT: Thompson, Penny P.  
; TITLE OF INVENTION: Human Zven Proteins  
; FILE REFERENCE: 99-81  
; CURRENT APPLICATION NUMBER: US/10/212,201A  
; CURRENT FILING DATE: 2002-08-02  
; PRIOR APPLICATION NUMBER: US/09/712,529  
; PRIOR FILING DATE: 2000-11-14  
; NUMBER OF SEQ ID NOS: 7

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
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; ORGANISM: Homo sapiens
US-10-212-201A-5

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QY 61 HPGSHKVPFFRKRGKHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
Db 61 HPGSHKVPFFRKRGKHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105

RESULT 3
US-10-212-355-5
; Sequence 5, Application US/10212355
; Patent No. 6828425
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/10/212,355
; CURRENT FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
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US-10-212-355-5

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Best Local Similarity 100.0%; Pred. No. 9.3e-59;
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Db 61 HPGSHKVPFFRKRGKHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105

RESULT 4
US-09-621-976-5350
; Sequence 5350, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 13335
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: SIGNAL
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US-09-621-976-5350

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QY 61 HPGSHKVPFFRKRGKHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105
Db 61 HPGSHKVPFFRKRGKHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105

RESULT 5
US-09-513-999C-4698
; Sequence 4698, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59 US2 REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4698
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: -19...-1
; OTHER INFORMATION: score 7.2
; OTHER INFORMATION: seq VSIMLLLVTVSDC/AV
US-09-513-999C-4698

Query Match      76.1%; Score 448; DB 4; Length 80;
Best Local Similarity 98.8%; Pred. No. 4.7e-43;
Matches 79; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 61 HPGSHKVPFFRKRGKHTCPC 80
Db 61 HPGSHKVPFFRKRGKHTCPC 80

RESULT 6
US-09-712-529-2
; Sequence 2, Application US/09712529
; Patent No. 6485938
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Bishop, Paul D.
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Thompson, Penny P.
; TITLE OF INVENTION: Human Zven Proteins
; FILE REFERENCE: 99-81
; CURRENT APPLICATION NUMBER: US/09/712,529
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/ CURRENT FILING DATE: 2000-11-14
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-712-529-2

Query Match      51.4%; Score 303; DB 4; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-26;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 10 MLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPF 69
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Qy 70 FRKKHHTCPCPLNLLCSRPFDGRYC 96
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 78 FGRMHHTCPCPLGLACLRTSFNRFC 104
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RESULT 7
US-10-212-201A-2
/ Sequence 2, Application US/10212201A
/ Patent No. 6756479
/ GENERAL INFORMATION:
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Bishop, Paul D.
/ APPLICANT: Whitmore, Theodore E.
/ APPLICANT: Thompson, Penny P.
/ TITLE OF INVENTION: Human Zven Proteins
/ FILE REFERENCE: 99-81
/ CURRENT APPLICATION NUMBER: US/10/212,201A
/ CURRENT FILING DATE: 2002-08-02
/ PRIOR FILING DATE: 2000-11-14
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 2
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-212-201A-2

Query Match      51.4%; Score 303; DB 4; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-26;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 10 MLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPF 69
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Qy 70 FRKKHHTCPCPLNLLCSRPFDGRYC 96
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Db 78 FGRMHHTCPCPLGLACLRTSFNRFC 104
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RESULT 8
US-10-212-355-2
/ Sequence 2, Application US/10212355
/ Patent No. 6828425
/ GENERAL INFORMATION:
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Bishop, Paul D.
/ APPLICANT: Whitmore, Theodore E.
/ APPLICANT: Thompson, Penny P.
/ TITLE OF INVENTION: Human Zven Proteins
/ FILE REFERENCE: 99-81
/ CURRENT APPLICATION NUMBER: US/10/212,355
/ CURRENT FILING DATE: 2002-08-02
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 3.0
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/ SEQ ID NO 2
/ LENGTH: 108
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-212-355-2

Query Match      51.4%; Score 303; DB 4; Length 108;
Best Local Similarity 55.2%; Pred. No. 1.2e-26;
Matches 48; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

Qy 10 MLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGECHPGSHKVPF 69
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Db 78 FGRMHHTCPCPLGLACLRTSFNRFC 104
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RESULT 9
US-09-161-241-14
/ Sequence 14, Application US/09161241
/ Patent No. 6344541
/ GENERAL INFORMATION:
/ APPLICANT: Bass, Michael B
/ APPLICANT: Sullivan, John K
/ APPLICANT: Theill, Lars E
/ APPLICANT: Wang, Daguang
/ TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
/ FILE REFERENCE: A-548
/ CURRENT APPLICATION NUMBER: US/09/161,241
/ CURRENT FILING DATE: 1998-09-25
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 14
/ LENGTH: 224
/ TYPE: PRT
/ ORGANISM: Human
US-09-161-241-14

Query Match      18.3%; Score 107.5; DB 3; Length 224;
Best Local Similarity 35.5%; Pred. No. 0.00025;
Matches 22; Conservative 5; Mismatches 32; Indels 3; Gaps 1;

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Qy 85 LC 86
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Db 201 LC 202
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RESULT 10
US-09-949-016-7146
/ Sequence 7146, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7146
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; LENGTH: 186  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-7146

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Best Local Similarity 31.5%; Pred. No. 0.00084;  
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 26 CERDVCGAGTCCCAISLWRLGLRMCTPLGREGEC-----HPGSHKVPPFRKRKHHTCPCL 81  
Db 110 CLRSSDCIEGFCARHF---TKICKPVLHQGEVCTKQRKKGSHGLEIFQR-----CDCA 161

QY 82 PNLCSRFDPGRY 94  
Db 162 KGLSCKVWKDATY 174

RESULT 11  
US-09-161-241-13  
; Sequence 13, Application US/09161241  
; Patent No. 6344541  
; GENERAL INFORMATION:  
; APPLICANT: Bass, Michael B  
; APPLICANT: Sullivan, John K  
; APPLICANT: Theill, Lars E  
; APPLICANT: Wang, Daquang  
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES  
; FILE REFERENCE: A-548  
; CURRENT APPLICATION NUMBER: US/09/161,241  
; CURRENT FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 207  
; TYPE: PRT  
; ORGANISM: Human  
US-09-161-241-13

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Best Local Similarity 31.5%; Pred. No. 0.00095;  
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

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Db 131 CLRSSDCIEGFCARHF---TKICKPVLHQGEVCTKQRKKGSHGLEIFQR-----CDCA 182

QY 82 PNLCSRFDPGRY 94  
Db 183 KGLSCKVWKDATY 195

RESULT 12  
US-09-161-241-12  
; Sequence 12, Application US/09161241  
; Patent No. 6344541  
; GENERAL INFORMATION:  
; APPLICANT: Bass, Michael B  
; APPLICANT: Sullivan, John K  
; APPLICANT: Theill, Lars E  
; APPLICANT: Wang, Daquang  
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES  
; FILE REFERENCE: A-548  
; CURRENT APPLICATION NUMBER: US/09/161,241  
; CURRENT FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 259  
; TYPE: PRT  
; ORGANISM: Human  
US-09-161-241-12

Query Match 17.3%; Score 102; DB 3; Length 259;  
Best Local Similarity 31.5%; Pred. No. 0.0012;  
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

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RESULT 13  
US-09-949-016-6872  
; Sequence 6872, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 6872  
; LENGTH: 259  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-6872

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Best Local Similarity 31.5%; Pred. No. 0.0012;  
Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;

QY 26 CERDVCGAGTCCCAISLWRLGLRMCTPLGREGEC-----HPGSHKVPPFRKRKHHTCPCL 81  
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QY 82 PNLCSRFDPGRY 94  
Db 235 KGLSCKVWKDATY 247

RESULT 14  
US-09-161-241-11  
; Sequence 11, Application US/09161241  
; Patent No. 6344541  
; GENERAL INFORMATION:  
; APPLICANT: Bass, Michael B  
; APPLICANT: Sullivan, John K  
; APPLICANT: Theill, Lars E  
; APPLICANT: Wang, Daquang  
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES  
; FILE REFERENCE: A-548  
; CURRENT APPLICATION NUMBER: US/09/161,241  
; CURRENT FILING DATE: 1998-09-25  
; NUMBER OF SEQ ID NOS: 78  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 259  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-161-241-11

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Best Local Similarity 31.5%; Pred. No. 0.0016;  
 Matches 23; Conservative 8; Mismatches 30; Indels 12; Gaps 3;  
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 Db 183 CLSSDCIDFGCCARHF-----TKICKPVLHQGEVCTQORKKSGHGLEIFOR-----CDCA 234  
 QY 82 PNLCSRFPDGRY 94  
 Db 235 KGLCKVWKDATY 247

RESULT 15  
 US-09-161-241-9  
 ; Sequence 9, Application US/09161241  
 ; Patent No. 6344541  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bass, Michael B  
 ; APPLICANT: Sullivan, John K  
 ; APPLICANT: Theill, Lars E  
 ; APPLICANT: Wang, Daguang  
 ; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES  
 ; FILE REFERENCE: A-548  
 ; CURRENT APPLICATION NUMBER: US/09/161,241  
 ; CURRENT FILING DATE: 1998-09-25  
 ; NUMBER OF SEQ ID NOS: 78  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 9  
 ; LENGTH: 350  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-161-241-9

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 Best Local Similarity 37.7%; Pred. No. 0.0025;  
 Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;  
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 Db 208 CDNRDCQPGCLCAFAQ---RGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDGALDR 264  
 QY 78 CPCLPNLLC 86  
 Db 265 CPCASGLLC 273

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 Job time : 43 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

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Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSMILLTVSDCA.....CSRFPGRYRCMDLKNVNF 105

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	589	100.0	105	9	US-09-989-727-371
5	589	100.0	105	9	US-09-989-731-371
6	589	100.0	105	9	US-09-989-732-371
7	589	100.0	105	9	US-09-991-073-371
8	589	100.0	105	9	US-09-990-442-371
9	589	100.0	105	9	US-09-991-163-371
10	589	100.0	105	9	US-09-993-604-371
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ALIGNMENTS

RESULT 1  
US-09-989-722-371  
; Sequence 371, Application US/09989722  
; Patent No. US20020072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tuma, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC63  
; CURRENT APPLICATION NUMBER: US/09/989, 722  
; CURRENT FILING DATE: 2001-11-19

1	PRIOR APPLICATION NUMBER: 60/049787	2	PRIOR FILING DATE: 1998-06-12
2	PRIOR FILING DATE: 1997-06-16	3	PRIOR APPLICATION NUMBER: 60/089440
3	PRIOR APPLICATION NUMBER: 60/062250	4	PRIOR FILING DATE: 1998-06-16
4	PRIOR FILING DATE: 1997-10-17	5	PRIOR APPLICATION NUMBER: 60/089512
5	PRIOR APPLICATION NUMBER: 60/065186	6	PRIOR FILING DATE: 1998-06-16
6	PRIOR FILING DATE: 1997-11-12	7	PRIOR APPLICATION NUMBER: 60/089514
7	PRIOR APPLICATION NUMBER: 60/065311	8	PRIOR FILING DATE: 1998-06-16
8	PRIOR FILING DATE: 1997-11-13	9	PRIOR APPLICATION NUMBER: 60/089532
9	PRIOR APPLICATION NUMBER: 60/066770	10	PRIOR FILING DATE: 1998-06-17
10	PRIOR FILING DATE: 1997-11-24	11	PRIOR APPLICATION NUMBER: 60/089538
11	PRIOR APPLICATION NUMBER: 60/075945	12	PRIOR FILING DATE: 1998-06-17
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15	PRIOR APPLICATION NUMBER: 60/083322	16	PRIOR FILING DATE: 1998-06-17
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17	PRIOR APPLICATION NUMBER: 60/084600	18	PRIOR FILING DATE: 1998-06-17
18	PRIOR FILING DATE: 1998-05-07	19	PRIOR APPLICATION NUMBER: 60/089653
19	PRIOR APPLICATION NUMBER: 60/087106	20	PRIOR FILING DATE: 1998-06-17
20	PRIOR FILING DATE: 1998-05-28	21	PRIOR APPLICATION NUMBER: 60/089801
21	PRIOR APPLICATION NUMBER: 60/087607	22	PRIOR FILING DATE: 1998-06-18
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23	PRIOR APPLICATION NUMBER: 60/087609	24	PRIOR FILING DATE: 1998-06-18
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25	PRIOR APPLICATION NUMBER: 60/087759	26	PRIOR FILING DATE: 1998-06-18
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47	PRIOR APPLICATION NUMBER: 60/088202	48	PRIOR FILING DATE: 1998-06-24
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61	PRIOR APPLICATION NUMBER: 60/088810	62	PRIOR FILING DATE: 1998-06-24
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63	PRIOR APPLICATION NUMBER: 60/088824	64	PRIOR FILING DATE: 1998-06-25
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; PRIOR FILING DATE: 1998-07-07
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGATRVISIMLLVTVSDCAVITGACERDVQCGAGTCCALSLWLRGLRMCTPLRGEGEC 60
DB 1 MRGATRVISIMLLVTVSDCAVITGACERDVQCGAGTCCALSLWLRGLRMCTPLRGEGEC 60

QY 61 HPGSHKVPFFRKRRKHTCPCLPNLLCSRFDPGRYRCSDMLKNINF 105
DB 61 HPGSHKVPFFRKRRKHTCPCLPNLLCSRFDPGRYRCSDMLKNINF 105

RESULT 2
US-09-989-723-371
; Sequence 371, Application US/09989723
; Patent No. US20020072092A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C62
; CURRENT APPLICATION NUMBER: US/09/989,723
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/065186
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478  
; PRIOR FILING DATE: 1998-07-02  
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; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09  
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Db 1 MEGATRVSIIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGLRMCTPLGREGEC 60  
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Db 61 HFGSHKVPFFRKRGKHTCTCPLNLLCSRFDPDGRYRCSDMLKNINF 105  
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RESULT 3  
US-09-989-279-371  
; Sequence 371, Application US/09989279  
; Patent No. US20020072496A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumaas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
;  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2730PIC56  
CURRENT APPLICATION NUMBER: US/09/989,279  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
PRIOR FILING DATE: 1997-06-16  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12



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; PRIOR APPLICATION NUMBER: 60/091478
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; PRIOR APPLICATION NUMBER: 60/091626
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; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match          100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRGATRVSIMLLAVTVSDCAVITGACERDVQCGAGTCCCAISLWLRGRLMCTPLGREGESC 60
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QY 61 HPGSHKVPFRKXKHTCTCLPNLLCSRPDPGRYRCSDMLKKNIF 105
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Db 61 HPGSHKVPFRKXKHTCTCLPNLLCSRPDPGRYRCSDMLKKNIF 105
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RESULT 4
US-09-989-727-371
; Sequence 371, Application US/09989727
; Patent No. US20020072497A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC65
; CURRENT APPLICATION NUMBER: US/09/989, 727
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-17
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; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: Acids Encoding the Same

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; Sequence 371, Application US/09989732
; Patent No. US20020123463A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas P.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C57
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Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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RESULT 7  
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; Sequence 371, Application US/09991073  
; Patent No. US20020127576A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC15  
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; CURRENT FILING DATE: 2001-11-14  
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; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      100.0%; Score 589; DB 9; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 8
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; Sequence 371, Application US/09990442
; Patent No. US20020132252A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C8
; CURRENT APPLICATION NUMBER: US/09/990,442
; CURRENT FILING DATE: 2001-11-14
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; PRIOR FILING DATE: 1998-07-09
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RESULT 9
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; Patent No. US20020132253A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
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; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC17
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67 PRIOR APPLICATION NUMBER: 60/092182  
68 PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 9; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.4e-53;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11  
US-09-990-456-371  
; Sequence 371, Application US/09990456  
; Patent No. US20020137890A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC22  
; CURRENT APPLICATION NUMBER: US/09/990,456  
; CURRENT FILING DATE: 2001-11-14  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 9; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.4e-53;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MRGATRVSIMLLLVTSVDCAVITGACERDVQCGAGTCCCAISLWLRGLRNMCTPLRGEGEC 60

QY 61 HPGSHKVPFRKRKHHTCPLNLLCSRPDGRYRCMDLKNINF 105  
Db 61 HPGSHKVPFRKRKHHTCPLNLLCSRPDGRYRCMDLKNINF 105

## RESULT 12

US-09-989-721-371  
; Sequence 371, Application US/09989721  
; Patent No. US20020142961A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumaas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC55  
; CURRENT APPLICATION NUMBER: US/09/989,721  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
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; PRIOR FILING DATE: 1998-07-07  
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; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 9; Length 105;

Best Local Similarity 100.0%; Pred. No. 1.4e-53;

Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13

US-09-992-598-371  
; Sequence 371, Application US/09992598  
; Patent No. US20020160384A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
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; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
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; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2730PIC20  
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US-09-886-242A-2  
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; Patent No. US20020172678A1  
; GENERAL INFORMATION:  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Watanabe, Colin  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: EG-VGF NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: GENENT 1516A  
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; PRIOR FILING DATE: 2000-09-07  
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; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: PCT/US00/00219  
; PRIOR FILING DATE: 2000-01-05  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: 1999-06-02  
; PRIOR APPLICATION NUMBER: US 09/709,238  
; PRIOR FILING DATE: 2000-11-08  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; US-09-886-242A-2

Query Match 100.0%; Score 589; DB 9; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.4e-53;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGATRVSIMLLVTSVSDCAVITGACRDRVCGAGTCCCAISLWRLGLRMCTPLRGEGSEC 60  
|||||  
Db 1 MRGATRVSIMLLVTSVSDCAVITGACRDRVCGAGTCCCAISLWRLGLRMCTPLRGEGSEC 60  
|||||

Qy 61 HPGSHKVPFFRKRRKHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105  
|||||  
Db 61 HPGSHKVPFFRKRRKHTCPCLPNLLCSRFPDGRYRCSMDLKNINF 105  
|||||

RESULT 15  
US-09-989-293A-371  
; Sequence 371, Application US/09989293A  
; Patent No. US20020177164A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Botstein, David  
; APPLICANT: Deenoyers, Luc  
; APPLICANT: Baton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher

;  
; PRIOR APPLICATION NUMBER: 60/088738  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088742  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088810  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088824  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088826  
; PRIOR FILING DATE: 1998-06-10  
; PRIOR APPLICATION NUMBER: 60/088858  
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; PRIOR APPLICATION NUMBER: 60/088861  
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; PRIOR FILING DATE: 1998-06-12  
; PRIOR APPLICATION NUMBER: 60/089440  
; PRIOR FILING DATE: 1998-06-16  
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; PRIOR FILING DATE: 1998-06-16  
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; PRIOR APPLICATION NUMBER: 60/089599  
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; PRIOR APPLICATION NUMBER: 60/089600  
; PRIOR FILING DATE: 1998-06-17  
; PRIOR APPLICATION NUMBER: 60/089653  
; PRIOR FILING DATE: 1998-06-17  
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; PRIOR FILING DATE: 1998-06-18  
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; PRIOR FILING DATE: 1998-06-18  
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; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090535  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090540

;  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090542  
; PRIOR FILING DATE: 1998-06-24  
; PRIOR APPLICATION NUMBER: 60/090557  
; PRIOR FILING DATE: 1998-06-24  
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; PRIOR FILING DATE: 1998-06-25  
; PRIOR APPLICATION NUMBER: 60/090690  
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; PRIOR APPLICATION NUMBER: 60/090694  
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; PRIOR APPLICATION NUMBER: 60/090862  
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; PRIOR FILING DATE: 1998-07-01  
; PRIOR APPLICATION NUMBER: 60/091478  
; PRIOR FILING DATE: 1998-07-02  
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; PRIOR FILING DATE: 1998-07-02  
; PRIOR APPLICATION NUMBER: 60/091978  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/091982  
; PRIOR FILING DATE: 1998-07-07  
; PRIOR APPLICATION NUMBER: 60/092182  
; PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 589; DB 9; Length 105;  
Best Local Similarity 100.0%; Pred. No. 1.4e-53;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRLMCTPLGRGEGEC 60  
Db 1 MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCCAISLWLRLMCTPLGRGEGEC 60  
Qy 61 HPGSHKVPFFRKHKHTCPLNLLCSRFPDGRYRCSMDLKNINF 105  
Db 61 HPGSHKVPFFRKHKHTCPLNLLCSRFPDGRYRCSMDLKNINF 105

Search completed: September 20, 2005, 13:13:09  
Job time : 170 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2005, 12:42:04 ; Search time 174 Seconds  
(without alignments)  
309.013 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSIMLLLVTVSDCA.....CSRFPDGRYRCSDMLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	589	100.0	105	1	PRK1_HUMAN	P58294 homo sapien
2	588	99.8	105	2	Q8TC69	Q8tc69 homo sapien
3	545	92.5	105	1	PRK1_RAT	Q8r414 rattus norv
4	432	73.3	81	2	Q8K457	Q8k457 mus musculu
5	318	54.0	108	2	Q863H4	Q863h4 bos taurus
6	310.5	52.7	81	1	VPRA_DENPO	P25687 dendroaspis
7	298.5	50.7	96	2	Q8JFQ0	Q8jfq0 bombina max
8	298	50.6	107	1	PRK2_RAT	Q8r413 rattus norv
9	298	50.6	128	2	Q863H5	Q863h5 bos taurus
10	287.5	48.8	96	1	BV8_BOMVA	Q9pw66 bombina var
11	282.5	48.0	129	1	PRK2_HUMAN	Q9hc23 homo sapien
12	277.5	47.1	128	1	PRK2_MOUSE	Q9qxu7 mus musculu
13	277.5	47.1	128	2	Q6V8J7	Q6v8j7 rattus norv
14	274.5	46.6	96	2	Q8JFE6	Q8jfe6 bombina max
15	273.5	46.4	96	2	Q8JFX8	Q8jfx8 bombina max
16	273.5	46.4	96	2	Q8JFY1	Q8jfy1 bombina max
17	269.5	45.8	96	2	Q8JFX9	Q8jfx9 bombina max
18	269.5	45.8	96	2	Q8JFY2	Q8jfy2 bombina max
19	266.5	45.2	96	2	Q8JFY2	Q8jfy2 bombina max
20	112	19.0	96	2	Q8UUX3	Q8uux3 gallus gall
21	108.5	18.4	221	2	Q8V8J3	Q8v8j3 mus musculu
22	107.5	18.3	224	1	DKK4_HUMAN	Q9ubt3 homo sapien
23	107.5	18.3	350	1	DKK3_CHICK	Q90839 gallus gall
24	104	17.7	255	2	Q9DDA4	Q9dda4 xenopus lae
25	102	17.3	259	1	DKK2_HUMAN	Q9ubz2 homo sapien
26	101	17.1	259	1	DKK2_MOUSE	Q9gyz8 mus musculu
27	101	17.1	259	2	Q8BFW0	Q8bfw0 m mus muscu
28	101	17.1	272	1	DKK1_MOUSE	Q54908 mus musculu
29	101	17.1	272	2	Q80UL5	Q80ul5 mus musculu
30	100.5	17.1	171	2	O43532	O43532 homo sapien
31	100.5	17.1	215	2	Q8N294	Q8n294 homo sapien

RESULT 1									
PRK1_HUMAN									
ID	PRK1_HUMAN	STANDARD;							
AC	P58234;								
DT	16-OCT-2001 (Rel. 40, Created)								
DT	16-OCT-2001 (Rel. 40, Last sequence update)								
DT	25-JAN-2005 (Rel. 46, Last annotation update)								
DE	Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF) (Mambakine) (UNQ600/PRO1186).								
DE	growth factor) (EG-VEGF) (Mambakine) (UNQ600/PRO1186).								
GN	Name=PROK1;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=21160229; PubMed=11259612;								
RA	Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.Y.;								
RT	"Identification of two prokineticin cDNAs: recombinant proteins								
RT	potently contract gastrointestinal smooth muscle.";								
RL	Mol. Pharmacol. 59:692-698(2001).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=21419730; PubMed=11528470; DOI=10.1038/35091000;								
RA	LeCouter J., Kowalewski J., Foster J., Hass P., Zhang Z.,								
RA	Dillard-Teim L., Frantz G., Rangell L., DeGuzman L., Keller G.-A.,								
RA	Peale F., Gurney A., Hillan K.J., Ferrara N.;								
RT	"Identification of an angiogenic mitogen selective for endocrine gland								
RT	endothelium.";								
RL	Nature 412:877-884 (2001).								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RX	Fraser C.;								
RT	"Mambakine, a snake venom related endocrine hormone that controls								
RT	macrophages.";								
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.								
RN	[4]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=22987296; PubMed=12975309; DOI=10.1101/gr.1293003;								
RA	Clark H.F., Gurney A.I., Abaya E., Baker K., Baldwin D., Brush J.,								
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,								
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,								
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,								
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,								
RA	Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,								
RA	Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.-H., Yansura D.,								
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,								
RT	"The secreted protein discovery initiative (SPDI), a large-scale								
RT	effort to identify novel human secreted and transmembrane proteins: a								
RT	bioinformatics assessment.";								
RL	Genome Res. 13:2265-2270(2003).								
RN	[5]								
RP	SEQUENCE OF 20-34.								

Q9ubp4 homo sapien  
Q9es33 rattus norv  
Q9qu9 mus musculu  
Q94907 homo sapien  
Q6pvu5 oryctolagus  
O57464 xenopus lae  
Q6pq81 homo sapien  
Q9pwh3 brachydanio  
Q8bu04 mus musculu  
Q642a8 rattus norv  
Q96397 chlamydomon  
Q9w690 brachydanio  
P42890 oryctolagus  
P87363 gallus gall

#### ALIGNMENTS

RESULT 1									
PRK1_HUMAN									
ID	PRK1_HUMAN	STANDARD;							
AC	P58234;								
DT	16-OCT-2001 (Rel. 40, Created)								
DT	16-OCT-2001 (Rel. 40, Last sequence update)								
DT	25-JAN-2005 (Rel. 46, Last annotation update)								
DE	Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF) (Mambakine) (UNQ600/PRO1186).								
DE	growth factor) (EG-VEGF) (Mambakine) (UNQ600/PRO1186).								
GN	Name=PROK1;								
OS	Homo sapiens (Human).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.								
OX	NCBI_TaxID=9606;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=21160229; PubMed=11259612;								
RA	Li M., Bullock C.M., Knauer D.J., Ehler F.J., Zhou Q.Y.;								
RT	"Identification of two prokineticin cDNAs: recombinant proteins								
RT	potently contract gastrointestinal smooth muscle.";								
RL	Mol. Pharmacol. 59:692-698(2001).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=21419730; PubMed=11528470; DOI=10.1038/35091000;								
RA	LeCouter J., Kowalewski J., Foster J., Hass P., Zhang Z.,								
RA	Dillard-Teim L., Frantz G., Rangell L., DeGuzman L., Keller G.-A.,								
RA	Peale F., Gurney A., Hillan K.J., Ferrara N.;								
RT	"Identification of an angiogenic mitogen selective for endocrine gland								
RT	endothelium.";								
RL	Nature 412:877-884 (2001).								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RX	Fraser C.;								
RT	"Mambakine, a snake venom related endocrine hormone that controls								
RT	macrophages.";								
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.								
RN	[4]								
RP	SEQUENCE FROM N.A.								
RX	MEDLINE=22987296; PubMed=12975309; DOI=10.1101/gr.1293003;								
RA	Clark H.F., Gurney A.I., Abaya E., Baker K., Baldwin D., Brush J.,								
RA	Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,								
RA	Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,								
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,								
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,								
RA	Seshagiri S., Simons L., Singh J., Smith V., Stinson J., Vagts A.,								
RA	Vandlen R., Watanabe C., Wicand D., Woods K., Xie M.-H., Yansura D.,								
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,								
RT	"The secreted protein discovery initiative (SPDI), a large-scale								
RT	effort to identify novel human secreted and transmembrane proteins: a								
RT	bioinformatics assessment.";								
RL	Genome Res. 13:2265-2270(2003).								
RN	[5]								
RP	SEQUENCE OF 20-34.								

RX PubMed=15340161; DOI=10.1110/ps.04682504;  
 RA Zhang Z., Henzel W.J.;  
 RT "Signal peptide prediction based on analysis of experimentally  
 RT verified cleavage sites.";  
 RL Protein Sci. 13:2819-2824(2004).  
 CC -I- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.  
 CC Induces proliferation, migration and fenestration (the formation  
 CC of membrane discontinuities) in capillary endothelial cells  
 CC derived from endocrine glands. Has little or no effect on a  
 CC variety of other endothelial and non-endothelial cell types.  
 CC -I- SUBCELLULAR LOCATION: Secreted.  
 CC -I- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary,  
 CC testis, adrenal and placenta.  
 CC -I- SIMILARITY: Belongs to the prokineticin family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; AF333024; AAK49918.1; -;  
 DR EMBL; AY029225; AAK33111.1; -;  
 DR EMBL; AY358683; AAQ89046.1; -;  
 DR HSSP; P25687; IIMT.  
 DR Genew; HGNC:18454; PROK1.  
 DR H-InvDB; HIX0000868; -;  
 DR MIM; 606233; -;  
 DR InterPro; IPR009523; Prokineticin.  
 DR Pfam; PR06607; Prokineticin; 1.  
 KW Direct protein sequencing; Growth factor; Mitogen; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 105 Prokineticin 1.  
 FT DISULFID 26 38 By similarity.  
 FT DISULFID 32 50 By similarity.  
 FT DISULFID 37 78 By similarity.  
 FT DISULFID 60 86 By similarity.  
 FT DISULFID 80 96 By similarity.  
 SQ SEQUENCE 105 AA; 11715 MW; C7E3FDE30EFB416A CRC64;  
  
 Query Match 100.0%; Score 589; DB 1; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 2,9e-52;  
 Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCAGTCCCAISLWLRGLRMCTPLRGEGEC 60  
 Db 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCAGTCCCAISLWLRGLRMCTPLRGEGEC 60  
  
 QY 61 HPGSHKVPFFRKHKHTCPLNLLCSRFPDGRYCSMDLKNINF 105  
 Db 61 HPGSHKVPFFRKHKHTCPLNLLCSRFPDGRYCSMDLKNINF 105  
  
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 Q8TC69 PRELIMINARY; PRT; 105 AA.  
 AC Q8TC69  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Prokineticin 1.  
 GN Names=PROK1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richardson S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schmerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2].  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Strausberg R.;  
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC025399; AAH25399.1; -;  
 DR HSSP; P25687; IIMT.  
 DR InterPro; IPR009523; Prokineticin.  
 DR Pfam; PF06607; Prokineticin; 1.  
 SQ SEQUENCE 105 AA; 11729 MW; E570FDE30EFB52D2 CRC64;  
  
 Query Match 99.8%; Score 588; DB 2; Length 105;  
 Best Local Similarity 99.8%; Pred. No. 3.7e-52;  
 Matches 104; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
 QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCAGTCCCAISLWLRGLRMCTPLRGEGEC 60  
 Db 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCAGTCCCAISLWLRGLRMCTPLRGEGEC 60  
  
 QY 61 HPGSHKVPFFRKHKHTCPLNLLCSRFPDGRYCSMDLKNINF 105  
 Db 61 HPGSHKVPFFRKHKHTCPLNLLCSRFPDGRYCSMDLKNINF 105  
  
 RESULT 3  
 PRK1\_RAT STANDARD; PRT; 105 AA.  
 ID PRK1\_RAT  
 AC Q8R414;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial  
 DE growth factor) (EG-VEGF).  
 GN Name=Prok1;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;  
 RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,  
 RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,  
 RA Inatomi N., Ohtaki T., Onda H., Fujino M.;  
 RT "Isolation and identification of EG-VEGF/prokineticins as cognate  
 RT ligands for two orphan G-protein-coupled receptors.";  
 RL Biochem. Biophys. Res. Commun. 293:396-402(2002).  
 CC -I- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.  
 CC Induces proliferation, migration and fenestration (the formation  
 CC of membrane discontinuities) in capillary endothelial cells  
 CC derived from endocrine glands. Has little or no effect on a  
 CC variety of other endothelial and non-endothelial cell types (By  
 CC similarity).

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CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the prokinectin family.
CC -----
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CC or send an email to license@isb-sib.ch)
CC -----
CC EMBL: AY089983; AM09104.1; -.
CC HSPF; P25687; 11MT.
CC RGD; 620898; Prok1.
CC InterPro; IPR009523; Prokinectin.
CC Pfam; PF06607; Prokinectin; 1.
CC Growth factor; Mitogen; Signal.
CC SIGNAL 1 19 Potential.
CC CHAIN 20 105 Prokinectin 1.
CC FT DISULFID 26 38 By similarity.
CC FT DISULFID 32 50 By similarity.
CC FT DISULFID 37 78 By similarity.
CC FT DISULFID 60 86 By similarity.
CC FT DISULFID 80 96 By similarity.
CC * SEQUENCE 105 AA; 11642 MW; 8DF0C42122B1C5B6 CRC64;
CC
CC Query Match 92.5%; Score 545; DB 1; Length 105;
CC Best Local Similarity 89.5%; Pred. No. 8.6e-48;
CC Matches 94; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
CC
CC Qy 1 MRGATRVSIIMLLVTSDCAVITGACERDVQCGAGTCCALISLWLRGRLMTCPLGREGGEC 60
CC Db 1 MRGAVQVFIMLLATVSDCAVITGACERDVQCGAGTCCALISLWLRGRLMTCPLGREGGEC 60
CC
CC Qy 61 HPGSHKVPFRKRKHHTCTPCPLNLLCSRFDPGRVRCSDMLKNINF 105
CC Db 61 HPGSHKVPFRKRKHHTCTPCSPSLSCSRFPDPGRVRCSDMLKNINF 105
CC
CC RESULT 4
CC Q8K457 PRELIMINARY; PRT; 81 AA.
CC ID Q8K457;
CC DT 01-OCT-2002 (TrEMBLrel. 22, Created)
CC DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
CC DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CC DE Prokinectin 1 (Fragment).
CC GN Name=Proki; Synonyms=PK1;
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=C57BL/6;
CC RX MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
CC RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
CC RA Weaver D.R., Leslie P.M., Zhou Q.Y.;
CC RT "Prokinectin 2 transmits the behavioural circadian rhythm of the
CC RT suprachiasmatic nucleus."
CC RL Nature 417:405-410(2002).
CC DR EMBL; AF487281; AA049573.1; -.
CC DR HSPF; P25687; 11MT.
CC DR MGD; MGI-2180370; Proki.
CC DR GO; GO:000576; C:extracellular; IDA.
CC DR GO; GO:000187; P:activation of MAPK; IDA.
CC DR GO; GO:0007623; P:circadian rhythm; TAS.
CC DR GO; GO:0008284; P:positive regulation of cell proliferation; IDA.
CC DR GO; GO:0045765; P:regulation of angiogenesis; IDA.
CC DR InterPro; IPR009523; Prokinectin.
CC DR Pfam; PF06607; Prokinectin; 1.
CC FT NON_TER 1 1
CC SQ SEQUENCE 81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;

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Query Match 73.3%; Score 432; DB 2; Length 81;
Best Local Similarity 87.7%; Pred. No. 2e-36;
Matches 71; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

Qy 25 ACERDVQCGAGTCCALISLWLRGRLMTCPLGREGGECHPGSHKVPFRKRKHHTCTPCPLNLL 84
Db 1 ACERDIQCGAGTCCALISLWLRGRLMTCPLGREGGECHPGSHKVPFLKRQHHTCTPCSPSL 60
Qy 85 LCSRFDPGRVRCSDMLKNINF 105
Db 61 LCSRFDPGRVRCSDMLKNINF 81

RESULT 5
Q863H4 PRELIMINARY; PRT; 108 AA.
ID Q863H4;
AC Q863H4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bv8/prokinectin 2-like protein splice variant.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
RA Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;
RT "The AVIT protein family."
RL EMO Rep. 4:469-473(2003).
DR EMBL; AX192558; AAP31907.1; -.
DR HSPF; P25687; 11MT.
DR InterPro; IPR009523; Prokinectin.
DR Pfam; PF06607; Prokinectin; 1.
DR SQ SEQUENCE 108 AA; 11672 MW; C00410399A9B215E CRC64;

Query Match 54.0%; Score 318; DB 2; Length 108;
Best Local Similarity 51.9%; Pred. No. 1e-24;
Matches 54; Conservative 15; Mismatches 27; Indels 8; Gaps 1;

Qy 1 MRGATRVSIIMLLV-----TVSDCAVITGACERDVQCGAGTCCCAISLWLRGRLMCTP 52
Db 1 MRSSRCARLLLLLLPPLLLTPPAGDAAVITGACDRDPQCGGGMCCCAVSLWVKSIRICTP 60
Qy 53 LGREGGECHPGSHKVPFRKRKHHTCTPCPLNLLCSRFDPGRVRC 96
Db 61 MGKVGDSCHPMTKVPFLGRMHHTCTCPLGLACSRTSFNRYTC 104

RESULT 6
VPRA DENPO
ID VPRA DENPO STANDARD; PRT; 81 AA.
AC P25687;
DT 01-MAY-1992 (Rel. 22, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Intestinal toxin 1 (MIT 1) (MIT1) (Venom protein A).
OS Dendroaspis polylepsis polylepsis (Black mamba).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Elapinae; Dendroaspis.
OC NCBI_TaxID=8620;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=81115818; PubMed=7461607;
RA Joubert F.J., Stridom D.J.;
RT "Snake venom. The amino acid sequence of protein A from Dendroaspis
RT polylepsis polylepsis (black mamba) venom."

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RL Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3;
RA Schweitz H., Pascaud P., Diochot S., Moirier D., Lazdunski M.;
RT "MIT1, a black mamba toxin with a new and highly potent activity on
RT intestinal contraction.";
RL FEBS Lett. 461:183-188(1998).
RN [3]
RN STRUCTURE BY NMR.
RC TISSUE=Venom;
RX MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
RA Boishovier J., Albrand J.-P., Blackledge M., Jaquinod M.,
RA Schweitz H., Lazdunski M., Marion D.;
RT "A structural homologue of colipase in black mamba venom revealed by
RT NMR floating disulphide bridge analysis.";
RL J. Mol. Biol. 283:205-219(1998).
CC -|- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the prokineticin family.
DR PDB; 1IMT; NMR; @=1-81.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KW 3D-structure; Direct protein sequencing; Toxin.
FT DISULFID 7 19
FT DISULFID 13 31
FT DISULFID 18 60
FT DISULFID 41 68
FT DISULFID 62 78
FT VARIANT 73 73 P -> Q (in protein A').
FT CONFLICT 18 18 C -> S (in Ref. 1).
FT CONFLICT 22 22 S -> C (in Ref. 1).
SQ SEQUENCE 81 AA; 8645 MW; 6C01368841572044 CRC64;

Query Match 52.7%; Score 310.5; DB 1; Length 81;
Best Local Similarity 62.8%; Pred. No. 4.5e-24;
Matches 49; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

QY 20 AVITGACERDVQCGAGTCCCAISLWLRGLMCTPLRGEGECHGSHKVPFFRKRK-HHTC 78
DB 1 AVITGACERDLOGKGTCCCAVSLWIKSVRVCTPVGTSGEDCHPASHKIPFGQKQVHHTC 60
QY 79 PCLPNLLCSRPFDGRYRC 96
DB 61 PCAPNLACVOTSPKPKFC 78

RESULT 7
ID Q8JFQ0 PRELIMINARY; PRT; 96 AA.
AC Q8JFQ0
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bv8 protein homolog 2.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin secretions;
RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00284-4;
RA Lai R., Liu H., Lee W.H., Zhang Y.;
RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina
RT maxima.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
DR EMBL; AF411091; AA003822.1; -.
DR HSSP; P25687; 1IMT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
SQ SEQUENCE 96 AA; 10198 MW; EC4EAA5EFE49B2F0 CRC64;

Query Match 50.7%; Score 298.5; DB 2; Length 96;
Best Local Similarity 53.6%; Pred. No. 8.8e-23;
Matches 52; Conservative 16; Mismatches 28; Indels 1; Gaps 1;

QY 1 MRGATRVSIMLLLVTVSDCAVTGACERDVQCGAGTCCCAISLWLRGLMCTPLRGEGREC 60
DB 1 MKCPAQIVLVLLVIAFSGAVITGACDRDVQCGSGTCCCAASLWSNRNIRFCVPLGNGGEC 60
QY 61 HPGSHKVPFFRKRKHHTCPCLPNLLCSRPFDGRYRC 97
DB 61 HPASHKVPYNGKRLSLCLPCKSLGTSKSGE-KFOCS 96

RESULT 8
PRK2_RAT STANDARD; PRT; 107 AA.
ID PRK2_RAT
AC Q8R413;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Prokineticin 2 precursor (PK2).
GN Name=Prok2; Synonyms=Bv8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
RA Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
RA Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
RA Inatomi N., Ohtaki T., Onda H., Fujino M.;
RT "Isolation and identification of EG-VGF/prokineticins as cognate
RT ligands for two orphan G-protein-coupled receptors.";
RL Biochem. Biophys. Res. Commun. 293:396-402(2002).
RN [2]
RP EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
RX MEDLINE=22024206; PubMed=12024206; DOI=10.1038/417405a;
RA Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
RA Weaver D.R., Leslie F.M., Zhou Q.-Y.;
RT "Prokineticin 2 transmits the behavioural circadian rhythm of the
RT suprachiasmatic nucleus.";
RL Nature 417:405-410(2002).
CC -|- FUNCTION: May function as an output molecule from the
CC suprachiasmatic nucleus (SCN) that transmits behavioral circadian
CC rhythm. May also function locally within the SCN to synchronize
CC output. Potentially contracts gastrointestinal (GI) smooth muscle (By
CC similarity).
CC -|- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -|- TISSUE SPECIFICITY: Expressed at high levels in testis and at
CC lower levels in brain, lung, ovary, spleen, thymus and uterus.
CC -|- INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light;
CC inhibited by period genes (PER1, PER2 and PER3) and cryptochrome
CC genes (CRY1 and CRY2) (Probable).
CC -|- SIMILARITY: Belongs to the prokineticin family.
CC -----
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CC -----
CC EMBL; AY089984; AA09105.1; -.
CC HSSP; P25687; 1IMT.
DR RGD; 620280; Bv8.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KW Biological rhythms; Neuropeptide; Signal.
FT SIGNAL 1 26 Potential.
FT CHAIN 27 107 Prokineticin 2.
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PT DISULFID 33 45 By similarity.
FT DISULFID 39 57 By similarity.
FT DISULFID 44 85 By similarity.
FT DISULFID 67 93 By similarity.
FT DISULFID 87 103 By similarity.
SQ SEQUENCE 107 AA; 11594 MW; BDFP316DCB5FED0 CRC64;

Query Match
Best Local Similarity 50.6%; Score 298; DB 1; Length 107;
Matches 47; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 10 MILLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGGECHPGSHKVPF 69
DB 17 LLTTPPAGDAVITGACDKDSQCGGMCACVSIWKSIRICTPMGQVGDSCPLTRKVPF 76
QY 70 FRKKRKHHTCPCLNLLCSRPDPGRYRC 96
DB 77 WGRMWHHTCPCLGACLRISFNRFIC 103

RESULT 9
Q863H5 PRELIMINARY; PRT; 128 AA.
AC Q863H5
* 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bv8/prokineticin 2-like protein.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
RA Kaser A., Winkmayr M., Lepperdinger G., Kreil G.;
RT "The AVIT protein family.";
RL EMBL Rep. 4:469-473(2003).
DR EMBL; AV192557; AAP31906.1; -.
DR HSP; P25687; ILMT.
DR GO; GO:0005576; C:extracellular; ISS.
DR GO; GO:0001664; F:G-protein-coupled receptor binding; ISS.
DR GO; GO:0000187; P:activation of MAPK; ISS.
DR GO; GO:0001525; P:angiogenesis; ISS.
DR GO; GO:0006916; P:anti-apoptosis; ISS.
DR GO; GO:0008283; P:cell proliferation; ISS.
DR GO; GO:0006935; P:chemotaxis; ISS.
DR GO; GO:0007204; P:cytosolic calcium ion concentration elevation; ISS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . ; ISS.
DR GO; GO:0006954; P:inflammatory response; ISS.
DR GO; GO:0019233; P:perception of pain; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . ; ISS.
DR GO; GO:0007283; P:spermatogenesis; ISS.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
SQ SEQUENCE 128 AA; 14290 MW; C22CDBDBE40483EC CRC64;

Query Match
Best Local Similarity 50.6%; Score 298; DB 2; Length 128;
Matches 54; Conservative 15; Mismatches 27; Indels 28; Gaps 2;

QY 1 MRGATRVSIMLLV-----TVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTP 52
DB 1 MRSRCARLLLLPPLLLTPPAGDAVITGACDRDPQCGGMCACVSIWKSIRICTP 60
QY 53 LGREGGECHPGSH-----KVPFRKRKHHTCPCLNLLCSRPDPG 92
DB 61 MGKVGDSCHPWTRKNHFGNGRQERKRKRKRKKVPLGRMHHTCPCLGLACSTSFN 120
QY 93 RYRC 96
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Db 121 RYTC 124

RESULT 10
Bv8_BOMVA STANDARD; PRT; 96 AA.
ID Bv8_BOMVA
AC Q9PW66;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Protein Bv8 precursor.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=8348;
RN [1]
RP SEQUENCE FROM N.A.; AND PARTIAL SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=99349621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0;
RA Mollay C., Wechselberger C., Mignogna G., Negri L., Melchiorri P.,
RA Barra D., Kreil G.;
RT Bv8, a small protein from frog skin and its homologue from snake
RT venom induce hyperalgesia in rats.;
RL Eur. J. Pharmacol. 374:189-196(1999).
CC -|- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
CC Induces hyperalgesia.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- SIMILARITY: Belongs to the prokineticin family.
CC -----
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CC -----
CC EMBL; AF168790; AAD45816.1; -.
CC HSP; P25687; ILMT.
CC InterPro; IPR009523; Prokineticin.
CC Pfam; PF06607; Prokineticin; 1.
CC Direct protein sequencing; Signal.
CC SIGNAL 1 19
CC CHAIN 20 96 Protein Bv8.
CC DISULFID 26 38 By similarity.
CC DISULFID 32 50 By similarity.
CC DISULFID 37 78 By similarity.
CC DISULFID 60 86 By similarity.
CC DISULFID 80 95 By similarity.
CC SEQUENCE 96 AA; 10102 MW; A12490A7437609B4 CRC64;

Query Match
Best Local Similarity 48.8%; Score 287.5; DB 1; Length 96;
Matches 49; Conservative 18; Mismatches 29; Indels 1; Gaps 1;

QY 1 MRGATRVSIMLLVTVSDCAVITGACERDVQCGAGTCCCAISLWRLGRLMCTPLGREGGE 60
DB 1 MKCFAQIVVLLLVIAESHGAVITGACDKDVQCGSGTCCCAASAWSRNIRFCIFLNSGDC 60
|||
QY 61 HPGSHKVPFRKRKHHTCPCLNLLCSRPDPGRYRC 97
DB 61 HPASHKVPYDVKRLSLCLPCSKGLTCKSGE-KFKCS 96

RESULT 11
PRK2_HUMAN STANDARD; PRT; 129 AA.
ID PRK2_HUMAN
AC Q9HC23;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Prokineticin 2 precursor (PK2) (protein Bv8 homolog).
GN Name=PROK2; Synonyms=BV8;

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DR	GO; GO:0007623;	P:circadian rhythm; IDA.
DR	GO; GO:0007204;	P:cytosolic calcium ion concentration elevation; ISS.
DR	GO; GO:0007186;	P:g-protein coupled receptor protein signalin. . ; ISS.
DR	GO; GO:0006954;	P:inflammatory response; ISS.
DR	GO; GO:0019233;	P:pain perception; ISS.
DR	GO; GO:0045887;	P:smooth muscle contraction; ISS.
DR	GO; GO:0007283;	P:spermatogenesis; ISS.
DR	pfam; PF06607;	P:prokineticin; I.
DR	InterPro; IPR009523;	P:prokineticin.
KW	Alternative splicing; Biological rhythms; Neuropeptide; Signal.	
FT	SIGNAL	1 26 Potential.
FT	CHAIN	27 128 Prokineticin 2.
FT	DISULFID	33 45 By similarity.
FT	DISULFID	39 57 By similarity.
FT	DISULFID	44 106 By similarity.
FT	DISULFID	67 114 By similarity.
FT	DISULFID	108 124 By similarity.
FT	VARSPLIC	74 94 Missing (in isoform 2).
FT	VARSPLIC	74 128 /FTId=VSP_005220.
FT	SHYANGQERRARRKRRKEVPFGWRMHHTCPLGGLAC	LRTSFNFRICLARK -> VSVCTGILGVPSH (in isoform 3).
FT	/FTId=VSP_005221.	
FT	SEQUENCE	128 AA; 14185 MW; 5F08BA177FDBB56C CRC64;
Query Match		47.1%; Score 277.5; DB 1; Length 128;
Best Local Similarity		40.7%; Pred. No. 1.6e-20;
Matches	50; Conservative	19; Mismatches 25; Indels 29; Gaps 2;
Qy	3 GATRVSIMLLLVTV-----SDCAVTGACERDVQCAGTCCAISSLWLRLGRMCTPLG S4	
Db	2 GDPCRAPLLLLLLLPLLPFPAGDAAVITGACDKSQCGGMCCAIVSWKSIRICTPMG 61	
Qy	55 REGECHPGSKH-----VFPERKKRKHKTCPCLPNLLCSRPDGR 93	
Db	62 QVGDSCHLTRKSHVANQGQRRAKRKRKKVEPFWGRRMHHTCPLGLACLRTS FNR 121	
Qy	94 YRC 96	
Db	122 FIC 124	
RESULT 13		
Q6V8J7		
ID	Q6V8J7 PRELIMINARY; PRT; 128 AA.	
AC	Q6V8J7;	
DT	05-JUL-2004 (TEMBLrel. 27, Created)	
DT	05-JUL-2004 (TEMBLrel. 27, Last sequence update)	
DT	05-JUL-2004 (TEMBLrel. 27, Last annotation update)	
DE	Prokineticin 2 beta.	
GN	Name=PK2beta;	
OS	Rattus norvegicus (Rat.).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	
OX	NCB1_TaxID=101116;	
ON	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAN=Sprague-Dawley;	
RA	Chen J., Sutton S., Kuei C., Wilson S.J., Lovenberg T.W., Liu C.;	
RL	Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.	
EMBL	AY348322; AAR06924.1; -	
DR	InterPro; IPR009523; Prokineticin.	
DR	pfam; PF06607; Prokineticin; 1.	
SEQ	SEQUENCE	128 AA; 14223 MW; 67050CC1A7D59466 CRC64;
Query Match		47.1%; Score 277.5; DB 2; Length 128;
Best Local Similarity		43.5%; Pred. No. 1.6e-20;
Matches	47; Conservative	16; Mismatches 24; Indels 21; Gaps 1;
Qy	10 MLLLVTSVCNVITGACERDVQCAGTCCAISSLWLRLGRMCTPLGREGECHPGSKH--- 66	
Db	17 LLTPPAGDAAVITGACDKSQCGGMCCAIVSWKSIRICTPMGQVGSCHPLTRKSHV 76	

```
QY 67 -----VPPFRKRKHHTCPCLNLLCSRPDPGRYRC 96
Db 77 ANGRQERRAKRRKRKEVPPFWRGMRHHHTCPCLPGLACLTSTFNRFC 124

RESULT 14
ID Q8JFE6 PRELIMINARY; PRT; 96 AA.
AC Q8JFE6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Bm8-a protein precursor [Bv8 protein homolog 1].
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shaw C.;
RT "Granular gland transcriptomes in stimulated amphibian skin
secretions.";
RL J. Biochem. 371:125-130(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin secretions;
RX MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
RA Lai R., Liu H., Lee W.H., Zhang Y.;
RT "Two novel Bv8-like peptides from skin secretions of the toad Bombina
maxima.";
RL Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
DR EMBL; AJ440230; CAD29340.1; -.
DR EMBL; AF411090; AAN03821.1; -.
DR HSSP; P25687; IIMT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT "CHAIN 20 96 Bm8-a protein.
SQ SEQUENCE 96 AA; 10117 MW; 2269AAC8654B18A6 CRC64;

Query Match 46.6%; Score 274.5; DB 2; Length 96;
Best Local Similarity 49.5%; Pred. No. 2.4e-20;
Matches 48; Conservative 17; Mismatches 31; Indels 1; Gaps 1;

QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEC 60
Db 1 MKCFAQIVVLLVIAFSGHAVITGVCDRDAQCGSGTCCAASAFSRNIRFCVPLGNNGEC 60
QY 61 HPGSHKVPFPRKRKHHTCPCLNLLCSRPDPGRYCS 97
Db 61 HPASHKVPYNGKRLSLCPCNTGLTCSKSGE-KFQCS 96

RESULT 15
Q8JFX8 PRELIMINARY; PRT; 96 AA.
AC Q8JFX8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bm8-f protein precursor.
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shaw C.;
RT "Granular gland transcriptomes in stimulated amphibian skin
secretions.";
```

```
RL J. Biochem. 371:125-130(2003).
DR EMBL; AJ440235; CAD29345.1; -.
DR HSSP; P25687; IIMT.
DR InterPro; IPR009523; Prokineticin.
DR Pfam; PF06607; Prokineticin; 1.
KW Signal.
FT SIGNAL 1 19 Potential.
FT CHAIN 20 96 Bm8-f protein.
SQ SEQUENCE 96 AA; 10058 MW; 2269A070FFE118A6 CRC64;

Query Match 46.4%; Score 273.5; DB 2; Length 96;
Best Local Similarity 50.5%; Pred. No. 3.1e-20;
Matches 49; Conservative 15; Mismatches 32; Indels 1; Gaps 1;

QY 1 MRGATRVSMILLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEC 60
Db 1 MKCFAQIVVLLVIAFSGHAVITGVCDRDAQCGSGTCCAASAFSRNIRFCVPLGNNGEC 60
QY 61 HPGSHKVPFPRKRKHHTCPCLNLLCSRPDPGRYCS 97
Db 61 HPASHKVPDGRKRLSLCPCNTGLTCSKSGE-KYQCS 96

Search completed: September 20, 2005, 12:58:58
Job time : 176 secs
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 20, 2005, 12:43:34 ; Search time 39 Seconds  
(without alignments)  
259.045 Million cell updates/sec

Title: US-10-692-299-2

Perfect score: 589

Sequence: 1 MRGATRVSMILLVTVSDCA.....CSRFPDGRVRCSDMLKNINF 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	100.5	17.1	350	2 JC7188	RBIC protein - hum
2	88.5	15.0	640	2 T08179	LRG5 protein - chl
3	83	14.1	1101	2 T16840	hypothetical prote
4	81	13.8	1964	2 T09059	notch4 - mouse
5	79	13.4	112	1 XLHU	colipase precursor
6	77.5	13.2	473	2 A56175	adhesive plaque pr
7	77	13.1	251	2 A55035	cysteine-rich prot
8	75.5	12.8	1574	2 T13954	MEGF6 protein - ra
9	75	12.7	734	2 JC4861	fertilin beta cha
10	75	12.7	2318	2 S45306	notch 3 protein -
11	75	12.7	2531	2 T31070	notch homolog - se
12	74	12.6	112	2 T51909	colipase precursor
13	74	12.6	1620	2 T27283	hypothetical prote
14	73	12.4	461	1 A35356	tumor necrosis fac
15	73	12.4	3075	2 S14458	laminin alpha-1 ch
16	72.5	12.3	643	2 T25473	hypothetical prote
17	72.5	12.3	2871	2 A55567	fibrillin I - bovi
18	72.5	12.3	3002	2 A47221	fibrillin I precu
19	72	12.2	1639	1 MMFPB2	laminin gamma-1 ch
20	71.5	12.1	591	2 I48141	acroganin - guine
21	71.5	12.1	601	2 B36346	fibulin 1 precurs
22	71.5	12.1	683	2 C36346	fibulin 1 precurs
23	71.5	12.1	1178	1 A39804	thrombospondin pre
24	71.5	12.1	1854	2 T13576	hypothetical prote
25	71	12.1	286	2 S34665	collagen, cuticula
26	71	12.1	593	1 GYHU	granulin precursor
27	70.5	12.0	1847	2 T18308	probable vitellog
28	70.5	12.0	2871	2 A55624	fibrillin-1 precu
29	69.5	11.8	802	2 T24293	hypothetical prote

30	69.5	11.8	949	2 T24294	hypothetical prote
31	69.5	11.8	2352	2 T30201	Notch homolog prot
32	69.5	11.8	4545	1 S25111	alpha-2-macroglobu
33	69	11.7	2918	2 A54105	fibrillin-2 precu
34	69	11.7	3133	2 S52093	hemocytin - silkw
35	69	11.7	3712	2 S18253	laminin alpha-1 ch
36	68.5	11.6	728	2 T50719	C-Delta-1 - chicke
37	68.5	11.6	850	2 T14450	serine/threonine k
38	68.5	11.6	884	2 T18649	hypothetical prote
39	68.5	11.6	1172	2 A42587	thrombospondin 2 p
40	68.5	11.6	1376	2 G00043	osteonidogen - hum
41	68	11.5	112	2 A46717	colipase precursor
42	68	11.5	345	2 T25138	hypothetical prote
43	68	11.5	358	2 T25137	hypothetical prote
44	68	11.5	427	1 GQHUN	nerve growth facto
45	68	11.5	547	2 A33901	mannosyl-oligosacc

ALIGNMENTS

RESULT 1

JC7188

RBIC protein - human

C;Species: Homo sapiens (man)

C;Date: 04-Mar-2000 #sequence\_revision 04-Mar-2000 #text\_change 11-May-2000

C;Accession: JC7188

R;Taugi, T.; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.

Biochem. Biophys. Res. Commun. 268, 20-24, 2000

A;Title: A RBIC gene shows down-regulation in human immortalized cells and human tumor-de

A;Reference number: JC7188; MUID:20119095; PMID:10652205

A;Accession: JC7188

A;Molecule type: mRNA

A;Residues: 1-350 <TSU>

A;Cross-references: DDBJ:AB034203

A;Experimental source: heart

C;Comment: This protein is a secreted glycoprotein for head induction in amphibian embryo

C;Genetics:

A;Gene: reic

C;Superfamily: human RBIC protein

C;Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor

Query Match 17.1%; Score 100.5; DB 2; Length 350;

Best Local Similarity 37.7%; Pred. No. 0.0089;

Matches 26; Conservative 3; Mismatches 29; Indels 11; Gaps 4;

QY 26 CERDVCGAGTCCATSLWRGL--RMCTPLGRGECH-PGSHKVPFRKRKH-----HT 77

Db 208 CNQRDCQFLCQAFQ---RGLLPVCTPLPVEGELCHDPASRLDLITWELEPDGALDR 264

QY 78 CPCPLNLLC 86

Db 265 CPCASGLLC 273

RESULT 2

T08179

LRG5 protein - Chlamydomonas reinhardtii

C;Species: Chlamydomonas reinhardtii

C;Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 09-Jul-2004

C;Accession: T08179

R;Gloeckner, G.; Beck, C.F.

submitted to the EMBL Data Library, October 1996

A;Description: Molecular characterization of a gene (LRG5) involved in blue light signal

A;Reference number: Z16399

A;Accession: T08179

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-640 <GLO>

A;Cross-references: UNIPROT:Q96397; EMBL:U73817; NID:g1644369; PID:g1644370

C;Genetics:

A;Gene: LRG5

```
Query Match      15.0%; Score 88.5; DB 2; Length 640;
Best Local Similarity 31.6%; Pred. No. 0.24; Indels 23; Gaps 4;
Matches 24; Conservative 5; Mismatches 24; Indels 23; Gaps 4;

QY 32 CGAGTCCATSLWRLGRLMCTPLGREGECHPGSHKVPFFRKXKHHTCPCLPNLLCSRF-- 89
DB 488 CTAGRC---WM---TCLPMWGGGTWPRLMTP-----SRTCACLIPTCCSRWLR 533

QY 90 -----PDGRYRCSM 98
DB 534 RWRGMAPGGRWRCSL 549

RESULT 3
T16840
Hypothetical protein T10E10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C:Accession: T16840
R:Geisels, C.
Submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.
A:Reference number: Z18588
A:Accession: T16840
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1101 <GEI>
A:Cross-references: UNIPROT:Q22378; EMBL:U93644; NID:g1049339; PID:g1049343; PIDN:AAA803
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7
Query Match      14.1%; Score 83; DB 2; Length 1101;
Best Local Similarity 24.4%; Pred. No. 1.3;
Matches 32; Conservative 9; Mismatches 40; Indels 50; Gaps 6;

QY 13 LVTVSDCAVITGACERDVQCGAGTCCCAISLWLRG----- 46
DB 749 LMSVQRCAMGIG-CPPGNQCEGVCPCPMCMSSGSIASSVCGMANSCPIGYICEGRGCCL 807

QY 47 --LRMCTPLGR-----EGECHPG-----SHKVPPFRKXKHHTCPCLPNLLCS 87
DB 808 EPLPLCPNGRASHMRCYRGACETPGYCTPLGGCLLSMEVPCTRSNAVCQSPNNVC- 866

QY 88 RFPDGRYRCSM 98
DB 867 --PSGA-SCTM 874

RESULT 4
T09059
notch4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T09059
R:Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; S
submitted to the EMBL Data Library, October 1997
A:Description: Sequence of the mouse major histocompatibility locus class III region.
A:Reference number: Z16543
A:Accession: T09059
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1964 <ROW>
A:Cross-references: UNIPROT:P31695; EMBL:AF030001; NID:g2564945; PID:g2564947
C:Genetics:
A:Gene: notch4
A:Map position: 17
A:Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67
1679/3; 1729/1; 1761/3
C:Suprafamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: receptor; signal transduction
F:514-545/Domain: EGF homology <EGF>
```

```
Query Match      13.8%; Score 81; DB 2; Length 1964;
Best Local Similarity 30.4%; Pred. No. 3.4; Indels 26; Gaps 5;
Matches 24; Conservative 7; Mismatches 22; Indels 26; Gaps 5;

QY 26 CERDVQ-----CGAGTCCCAISLWRLGRLMCTPLGREGECHPGSHKVPFFRKXKH 76
DB 188 CERDINECFLEPGCPQGTSCHTNL---GSYQCLCPVGQEGPQC-----KLRKG 233

QY 77 TCP---CLPNLLCSRFPDG 92
DB 234 ACPGSGCLNGGTQCLVPEG 252

RESULT 5
XLHU
Colipase precursor [validated] - human
N:Alternate names: procolipase
C:Species: Homo sapiens (man)
C:Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C:Accession: A42568; A33949; A03163
R:Sims, H.F.; Lowe, M.E.
Biochemistry 31, 7120-7125, 1992
A:Title: The human colipase gene: isolation, chromosomal location, and tissue-specific e
A:Reference number: A42568; MUID:92353041; PMID:1643046
A:Accession: A42568
A:Molecule type: DNA
A:Residues: 1-112 <SIM>
A:Cross-references: UNIPROT:P04118; GB:M95529; NID:g180842; PIDN:AAB05818.1; PID:g1483624
A:Note: sequence extracted from NCBI backbone (NCBIN:110576, NCBIN:110578, NCBIN:110580)
R:Lowe, M.E.; Rosenblum, J.L.; McEwen, P.; Strauss, A.W.
Biochemistry 29, 823-828, 1990
A:Title: Cloning and characterization of the human colipase cDNA.
A:Reference number: A33949; MUID:90248429; PMID:2337598
A:Accession: A33949
A:Molecule type: mRNA
A:Residues: 1-112 <LOW>
A:Cross-references: GB:J02883; NID:g180885; PIDN:AAA52054.1; PID:g180886
A:Note: evidence of partial N-glycosylation, possibly at Asn-43
R:Sternby, B.; Engstrom, A.; Hellman, U.; Viher, A.M.; Sternby, N.H.; Borgstrom, B.
Biochim. Biophys. Acta 784, 75-80, 1984
A:Title: The primary sequence of human pancreatic colipase.
A:Reference number: A90652; MUID:84104937; PMID:6691986
A:Accession: A03163
A:Molecule type: protein
A:Residues: 23-108 <STE>
C:Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 stoic
se the enzyme is washed off by bile salts, which are known to have an inhibitory effect c
C:Genetics:
A:Gene: GDB:CLPS
A:Cross-references: GDB:127277; OMIM:120105
A:Map position: 6pter-6p21.1
A:Introns: 28/3; 69/3
C:Suprafamily: colipase
C:Keywords: lipid digestion; lipid hydrolysis; pancreas
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-22/Domain: amino-terminal propeptide #status predicted <APP>
F:23-108/Product: colipase #status experimental <NAI>
F:109-112/Domain: carboxyl-terminal propeptide #status predicted <CPP>
F:34-104,40-56,44-80,45-78,66-86/Disulfide bonds: #status predicted
F:69,72,75,76/Binding site: micellar substrate (Lys, Tyr, Tyr) #status predicted

Query Match      13.4%; Score 79; DB 1; Length 112;
Best Local Similarity 28.4%; Pred. No. 0.5;
Matches 31; Conservative 9; Mismatches 45; Indels 24; Gaps 6;

QY 9 IMLLVTVSDCAVITG-----ACERDVQCGAGTCCCAISLWRLGRLMCTPLGRE 56
DB 5 LILLVALSVAAAPGPGIINLENGELCMNSAQ-C-KNCCCHSSAL-GLARCTSMASE 62

QY 57 GBECHPGSHKVPFFRKXKHHTCPCLPNLLCSRFPDGGRYRCSDMLKNINF 105
DB 63 NSEC---SVKTLV---GIYKPCPCERGLTC----EGDKTIVGSITNTNF 101
```

RESULT 6

A56175

adhesive plaque protein Mgf12 precursor - Mediterranean mussel

C:Species: Mytilus galloprovincialis (Mediterranean mussel)

C>Date: 27-Apr-1995 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004

C:Accession: A56175

R;Inoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.

J. Biol. Chem. 270, 6698-6701, 1995

A:Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth factor

A:Reference number: A56175; MUID:95204464; PMID:7896812

A:Accession: A56175

A:Molecule type: mRNA

A:Residues: 1-473 <INO>

A:CROSS-references: UNIPROT:Q25464; GB:D43794; NID:g602767; PIDN:BAA07852.1; PID:d100843

C:Keywords: duplication

F:1-17/Domain: signal sequence #status predicted <SIG>

F:387-419/Domain: EGF homology <EGF1>

F:429-460/Domain: EGF homology <EGF>

F:23,36,43,56,75,382,424,455,468,473/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #

Query Match 13.2% Score 77.5; DB 2; Length 473;

Best Local Similarity 31.2%; Pred. No. 2.4; Mismatches 23; Indels 19; Gaps 7;

Matches 24; Conservative 11;

QY 26 CERDVOQGAGTCCAISLWLRLMCTPLRGEGECH-PGSHKVPFFPKRKHHC---PCL 81

DB 117 CERNV-CSPNPC-----KNGKCSPLGKTGYKTCGGYTCP---RCEVHACKNPCK 165

QY 82 PNLLCSRFDPGR--YRC 96

DB 166 NKGRC--FPDGKTYKC 180

RESULT 7

A55035

cysteine-rich protein CRP1 - earthworm (Enchytraeus buchholzi)

C:Species: Enchytraeus buchholzi

C>Date: 14-Nov-1994 #sequence\_revision 03-Nov-1995 #text\_change 09-Jul-2004

C:Accession: A55035; S45034

R;Willuhn, J.; Schmitt-Wrede, H.P.; Greven, H.; Wunderlich, F.

J. Biol. Chem. 269, 24688-24691, 1994

A:Title: cDNA cloning of a cadmium-inducible mRNA encoding a novel cysteine-rich, non-me

A:Reference number: A55035; MUID:95014230; PMID:7929141

A:Accession: A55035

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-251 <WIL>

A:CROSS-references: UNIPROT:Q24774; EMBL:X79344; NID:g488802; PIDN:CAA55899.1; PID:g488488

C:Superfamily: ultra-high-sulfur keratin

Query Match 13.1% Score 77; DB 2; Length 251;

Best Local Similarity 30.9%; Pred. No. 1.6;

Matches 25; Conservative 7; Mismatches 45; Indels 4; Gaps 3;

QY 17 SDCAVITGACERDVQCGAGTCCAISLWLRLMCTPLRGEGECHPGSHKVPFFPKRKH 76

DB 77 SQCKEKGECKG--CKEG--CCAPKGVAGSCGCKEKGCKPCTRCGTCGTCGVE 133

QY 77 TCPCLPNLLCSRFDPGRYRCS 97

DB 134 DCPGSPCKCEK-GDCKVNC 153

RESULT 8

T13954

MEGF6 protein - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004

C:Accession: T13954

R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.

Genomics 51, 27-34, 1998



A;Residues: 1-2318 <LAR>  
A;Cross-references: UNIPROT:Q61982; EMBL:X74760; NID:g483580; PIDN:CAA52776.1; PID:g483580  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology  
F;163-195/Domain: EGF homology <EGF1>  
F;474-505/Domain: EGF homology <EGF2>  
F;854-885/Domain: EGF homology <EGF2>  
F;1839-1871/Domain: ankyrin repeat homology <AN1>  
F;1872-1904/Domain: ankyrin repeat homology <AN2>  
F;1906-1938/Domain: ankyrin repeat homology <AN3>  
F;1939-1971/Domain: ankyrin repeat homology <AN4>  
F;1972-2004/Domain: ankyrin repeat homology <AN5>

Query Match 12.7%; Score 75; DB 2; Length 2318;  
Best Local Similarity 28.1%; Pred. No. 16;  
Matches 25; Conservative 5; Mismatches 25; Indels 34; Gaps 5;

QY 19 CAVITGACERDVQCGAGTCAISLWLRGLRMCTPLGREGREC-----60  
Db 1287 CERVARS-RELQCPVGPQQQT--ARGPRCACPPGLSGPSCRSPSGATNASCASA 1343

QY 61 ---HPGS----HKVPFRKRKHHTCPCLP 82  
Db 1344 PCLHGSGCLPVQSVPFPR-----CVCAP 1366

RESULT 11  
T31070  
notch homolog - sea urchin (*Lytechinus variegatus*)  
C;Species: *Lytechinus variegatus* (variegated urchin)  
C;Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 31-Jan-2000  
C;Accession: T31070  
R;Sherwood, D.R.; McClay, D.R.  
Development 124, 3363-3374, 1997  
A;Title: Identification and localization of a sea urchin Notch homologue: insights into  
A;Reference number: Z20966; MUID:97454256; PMID:9310331  
A;Accession: T31070  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-2531 <SHE>  
A;Cross-references: EMBL:AF00634; NID:g2570350; PID:g2570351; PIDN:AA82088.1  
C;Superfamily: notch protein; ankyrin repeat homology; EGF homology

Query Match 12.7%; Score 75; DB 2; Length 2531;  
Best Local Similarity 29.9%; Pred. No. 17;  
Matches 23; Conservative 8; Mismatches 32; Indels 14; Gaps 5;

QY 22 ITGACERDVQCGAGTCCAI--SLWLRGLRMCTPLGREGECHPGSHKVPFRKRKHHTCP 79  
Db 120 VDNVCKLEPCQNGTCLRTSLMDYEC-FCITP-ANTGENCTDDNHCV-----SNP 168

QY 80 CLPNLLCSRPFDGRYRC 96  
Db 169 CLNGAVCTSSSDG-YSC 184

RESULT 12  
I51909  
colipase precursor - rat  
N;Alternate names: procoplipase  
C;Species: *Rattus norvegicus* (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I51909; A34623  
R;Payne, R.M.; Sims, H.F.; Jennens, M.L.; Lowe, M.E.  
Am. J. Physiol. 266, G914-G921, 1994  
A;Title: Rat pancreatic lipase and two related proteins: enzymatic properties and mRNA  
A;Reference number: I51909; MUID:94262798; PMID:8203536  
A;Accession: I51909  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-112 <PAY>  
A;Cross-references: UNIPROT:P17084; GB:M58370; NID:g203504; PIDN:AAA20505.1; PID:g203505  
R;Wicker, C.; Puigserver, A.  
Biochem. Biophys. Res. Commun. 167, 130-136, 1990

A;Title: Rat pancreatic colipase mRNA: nucleotide sequence of a cDNA clone and nutrition  
A;Reference number: A34623; MUID:90179738; PMID:2129524  
A;Accession: A34623  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-17, 'V', 19-112 <WIC>  
A;Cross-references: GB:M33333; NID:g203502; PIDN:AAA40943.1; PID:g203503  
C;Superfamily: colipase  
C;Keywords: lipid digestion; lipid hydrolysis; pancreas  
F;1-17/Domain: signal sequence #status predicted <SIG>  
F;18-112/Product: colipase #status predicted <MAT>

Query Match 12.6%; Score 74; DB 2; Length 112;  
Best Local Similarity 25.8%; Pred. No. 1.6;  
Matches 24; Conservative 10; Mismatches 39; Indels 20; Gaps 4;

QY 6 RVSIMLLLVTVGDCAVITS-----ACERDVQCGAGTCCCAISLWLRGLRMCTPL 53  
Db 2 KVLVLLVTLVAVAAPGPRGLFINLEDGEICVNSMQC-KSRCCQHDITL-GIARCTHK 59

QY 54 GREGECHPGSHKVPFRKRKHHTCPCLPNLLC 86  
Db 60 AMENSECSPKTLGIYYR-----CPCERGLTC 86

RESULT 13  
T27283  
hypothetical protein Y64G10A.f - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C;Accession: T27283  
R;Ainscough, R.  
submitted to the EMBL Data Library, September 1999  
A;Reference number: Z20336  
A;Accession: T27283  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-1620 <WIL>  
A;Cross-references: EMBL:AL110498; NID:e1542303; PIDN:CAB54471.1; CESP:Y64G10A.f  
A;Experimental source: clone Y64G10A  
C;Genetics:  
A;Gene: CESP:Y64G10A.f  
A;Introns: 77/1; 116/1; 198/1; 282/1; 365/1; 425/1; 466/1; 548/1; 559/1; 601/1; 625/1; 71

Query Match 12.6%; Score 74; DB 2; Length 1620;  
Best Local Similarity 27.5%; Pred. No. 15;  
Matches 22; Conservative 4; Mismatches 16; Indels 38; Gaps 4;

QY 16 VSDCAVITGACERDVQCGAG-----TCCCAISLWLRGLRMCTPLGREGECHPGSHKVP 68  
Db 1114 VARCDHVTGEC-----RCPAGWTGPDCTSC-----PLGRHGEGC----- 1148

QY 69 FFRKRKHHTCPCLPNLLCSR 88  
Db 1149 -----RHSCQCSNGASCDSR 1162

RESULT 14  
A35356  
tumor necrosis factor receptor 2 precursor [validated] - human  
N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2  
C;Species: *Homo sapiens* (man)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A35356; A36475; A48416; A36667; B35010; I38094  
R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K.  
Science 248, 1019-1023, 1990  
A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and  
A;Reference number: A35356; MUID:90260639; PMID:2160731  
A;Accession: A35356  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-461 <SMI>  
A;Cross-references: UNIPROT:P20333; GB:M32315; NID:gl89185; PIDN:AAA59929.1; PID:gl89186



R;Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990

A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occurring soluble form of the ligand

A;Reference number: A36475; MUID:91045991; PMID:2172983

A;Accession: A36475

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-195, 'R', 197-461 <KOH>

A;Cross-references: GB:M55994; GB:M38549; NID:G339757; PIDN:AAA36755.1; PID:G339758

R;Demic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990

A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular, domains

A;Reference number: A48416; MUID:91370690; PMID:1966549

A;Accession: A48416

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 23-461 <DEM>

A;Cross-references: GB:S63368; NID:G235648; PIDN:AAB19824.1; PID:G235649

R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990

A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of its expression in human monocytes

A;Reference number: A36007; MUID:90349572; PMID:2166946

A;Accession: A36007

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>

A;Cross-references: GB:M35957; NID:G339751; PIDN:AAA63262.1; PID:G339752

R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20139, 1990

A;Title: Purification and partial amino acid sequence analysis of two distinct tumor necrosis factor receptors

A;Reference number: A23666; MUID:91056048; PMID:2173696

A;Accession: A23666

A;Status: preliminary

A;Molecule type: protein

A;Residues: 23-40;65-69;136-141;300-306 <LOE>

R;Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990

A;Title: Tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct receptors

A;Reference number: A35010; MUID:90110215; PMID:2153136

A;Accession: B35010

A;Status: preliminary

A;Molecule type: protein

A;Residues: 27-31 <ENG>

R;Kuhnert, P.; Kemper, O.; Wallach, D. Gene 150, 381-386, 1994

A;Title: Cloning, sequencing and partial functional characterization of the 5' region of the human TNF receptor

A;Reference number: I38094; MUID:95121934; PMID:7821811

A;Accession: I38094

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-37 <RES>

A;Cross-references: EMBL:X80021; NID:G666044; PIDN:CAA56324.1; PID:G825701

C;Genetics:

A;Gene: GDB:TNFR2

A;Cross-references: GDB:125914; OMIM:191191

A;Map position: 1p36.2-1p36.2

A;Introns: 26/3

A;Note: the list of introns is incomplete

C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homologous

C;Keywords: duplication; glycoprotein; receptor; transmembrane protein

F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>

F;40-76/Domain: NGF receptor repeat homology <NG1>

F;78-119/Domain: NGF receptor repeat homology <NG2>

F;120-162/Domain: NGF receptor repeat homology <NG3>

F;164-201/Domain: NGF receptor repeat homology <NG4>

F;262-279/Domain: transmembrane #status predicted <TMN>

F;280-461/Domain: intracellular #status predicted <INT>

F;171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.4%; Score 73; DB 1; Length 461;  
Best Local Similarity 29.5%; Pred. No. 6.6;

Query Match	12.4%;	Score 73;	DB 1;	Length 461;
Best Local Similarity	29.5%;	Pred. No. 6.6;		

F:1362-1400/Domain: laminin-type EGF-like homology #status atypical <LE17>  
F:1403-1449/Domain: laminin-type EGF-like homology <LE18>  
F:1452-1506/Domain: laminin-type EGF-like homology <LE19>  
F:1509-1553/Domain: laminin-type EGF-like homology <LE20>  
F:1554-2125/Domain: I/II, heptad repeats <DOM2>  
F:2116-2120/Region: cell adhesion #status predicted  
F:2126-3075/Domain: G <DOMG>  
F:2142-2300/Domain: laminin G repeat homology <LG1>  
F:2329-2484/Domain: laminin G repeat homology <LG2>  
F:2510-2676/Domain: laminin G repeat homology <LG3>  
F:2534-2536/Region: cell attachment (R-G-D) motif  
F:2739-2888/Domain: laminin G repeat homology <LG4>  
F:2916-3073/Domain: laminin G repeat homology <LG5>  
F:38,164,555,665,763,801,838,926,952,1045,1407,1579,1596,1678,1689,1698,1717,1804,1894,1  
rate (Asn) (covalent) #status predicted  
F:297-305/Disulfide bonds: #status predicted

Query Match 12.4%; Score 73; DB 2; Length 3075;  
Best Local Similarity 23.0%; Pred. No. 32;  
Matches 23; Conservative 10; Mismatches 35; Indels 32; Gaps 4;

QY 19 CAVITGACERDVQCGAGTCCAISLWLRGLRMCTPL-----GREGECH-----P 62  
DB 1056 CDVVTGHQCKSKFGGRACDQCGLGYRDFPDCVPCDCLRGTSGDACNLEQGLCGCVET 1115  
QY 63 GSHKVPFFRRKHHTCPCLPNLL---CSRFPDGRYRCSD 99  
DB 1116 GA-----CPCKENVFGQCNECREGTFAIRAD 1142

Search completed: September 20, 2005, 12:59:43  
Job time : 40 secs